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1
A

2 32
GTT TTA CAC CAT CAC CAA AAC CCA GAA TTT TAT GAT GAG ATT AAA ATA GAG TTG CCC ACT
val leu his his his gln asn pro glu phe tyr asp glu ile lys ile glu leu pro thr

62 92
CAG CTG CAT GAA AAG CAC CAC CTG TTG CTC ACA TTC TTC CAT GTC AGC TGT GAC AAC TCA
gln leu his glu lys his his leu leu leu thr phe phe his val ser cys asp asn ser

122 152
AGT AAA GGA AGC ACG AAG AAG AGG GAT GTC GTT GAA ACC CAA GTT GGC TAC TCC TGG CTT
ser lys gly ser thr lys lys arg asp val val glu thr gln val gly tyr ser trp leu

182 212
CCC CTC CTG AAA GAC GGA AGG GTG GTG ACA AGC GAG CAG CAC ATC CCG GTC TCG GCG AAC
pro leu leu lys asp gly arg val val thr ser glu gln his ile pro val ser ala asn

242 272
CTT CCT TCG GGC TAT CTT GGC TAC CAA GAG CTT GGG ATG GGC AGG CAT TAT GGT CCG GAA
leu pro ser gly tyr leu gly tyr gln glu leu gly met gly arg his tyr gly pro glu

302 332
ATT AAA TGG GTA GAT GGA GGC AAG CCA CTG CTG AAA ATT TCC ACT CAT CTG GTT TCT ACA
ile lys trp val asp gly gly lys pro leu leu lys ile ser thr his leu val ser thr

362 392
GTG TAT ACT CAG GAT CAG CAT TTA CAT AAT TTT TTC CAG TAC TGT CAG AAA ACC GAA TCT
val tyr thr gln asp gln his leu his asn phe phe gln tyr cys gln lys thr glu ser

422 452
GGA GCC CAA GCC TTA GGA AAC GAA CTT GTA AAG TAC CTT AAG AGT CTG CAT GCG ATG GAA
gly ala gln ala leu gly asn glu leu val lys tyr leu lys ser leu his ala met glu

482 512
GGC CAC GTG ATG ATC GCC TTC TTG CCC ACT ATC CTA AAC CAG CTG TTC CGA GTC CTC ACC
gly his val met ile ala phe leu pro thr ile leu asn gln leu phe arg val leu thr

542 572
AGA GCC ACA CAG GAA GAA GTC GCG GTT AAC GTG ACT CGG GTC ATT ATT CAT GTG GTT GCC
arg ala thr gln glu glu val ala val asn val thr arg val ile ile his val val ala

602 632
CAG TGC CAT GAG GAA GGA TTG GAG AGC CAC TTG AGG TCA TAT GTT AAG TAC GCG TAT AAG
gln cys his glu glu gly leu glu ser his leu arg ser tyr val lys tyr ala tyr lys

662 692
GCT GAG CCA TAT GTT GCC TCT GAA TAC AAG ACA GTG CAT GAA GAA CTG ACC AAA TCC ATG
ala glu pro tyr val ala ser glu tyr lys thr val his glu glu leu thr lys ser met

FIG. 1

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722 752
ACC ACG ATT CTC AAG CCT TCT GCC GAT TTC CTC ACC AGC AAC AAA CTA CTG AGG TAC TCA
thr thr ile leu lys pro ser ala asp phe leu thr ser asn lys leu leu arg tyr ser

782 812
TGG TTT TTC TTT GAT GTA CTG ATC AAA TCT ATG GCT CAG CAT TTG ATA GAG AAC TCC AAA
trp phe phe phe asp val leu ile lys ser met ala gln his leu ile glu asn ser lys

842 |Cadherin Cleavage| 872
GTT AAG TTG CTG CGA AAC CAG AGA TTT CCT GCA TCC TAT CAT CAT GCA GCG GAA ACC GTT
val lys leu leu arg asn gln arg phe pro ala ser tyr his his ala ala glu thr val

902 932
GTA AAT ATG CTG ATG CCA CAC ATC ACT CAG AAG TTT GGA GAT AAT CCA GAG GCA TCT AAG
val asn met leu met pro his ile thr gln lys phe gly asp asn pro glu ala ser lys

962 992
AAC GCG AAT CAT AGC CTT GCT GTC TTC ATC AAG AGA TGT TTC ACC TTC ATG GAC AGG GGC
asn ala asn his ser leu ala val phe ile lys arg cys phe thr phe met asp arg gly

1022 1052
TTT GTC TTC AAG CAG ATC AAC AAC TAC ATT AGC TGT TTT GCT CCT GGA GAC CCA AAG ACC
phe val phe lys gln ile asn asn tyr ile ser cys phe ala pro gly asp pro lys thr

1082 1112
CTC TTT GAA TAC AAG TTT GAA TTT CTC CGT GTA GTG TGC AAC CAT GAA CAT TAT ATT CCG
leu phe glu tyr lys phe glu phe leu arg val val cys asn his glu his tyr ile pro

1142 1172
TTG AAC TTA CCA ATG CCA TTT GGA AAA GGC AGG ATT CAA AGA TAC CAA GAC CTC CAG CTT
leu asn leu pro met pro phe gly lys gly arg ile gln arg tyr gln asp leu gln leu

1202 1232 |Cadherin EC
GAC TAC TCA TTA ACA GAT GAG TTC TGC AGA AAC CAC TTC TTG GTG GGA CTG TTA CTG AGG
asp tyr ser leu thr asp glu phe cys arg asn his phe leu val gly leu leu leu arg

xxx| 1292
GAG GTG GGG ACA GCC CTC CAG GAG TTC CGG GAG GTC CGT CTG ATC GCC ATC AGT GTG CTC
glu val gly thr ala leu gln glu phe arg glu val arg leu ile ala ile ser val leu

1322 1352
AAG AAC CTG CTG ATA AAG CAT TCT TTT GAT GAC AGA TAT GCT TCA AGG AGC CAT CAG GCA
lys asn leu leu ile lys his ser phe asp asp arg tyr ala ser arg ser his gln ala

1382 1412/471
AGG ATA GCC ACC CTC TAC CTG CCT CTG TTT GGT CTG CTG ATT GAA AAC GTC CAG CGG ATC
arg ile ala thr leu tyr leu pro leu phe gly leu leu ile glu asn val gln arg ile

1442 1472
AAT GTG AGG GAT GTG TCA CCC TTC CCT GTG AAC GCG GGC ATG ACC GTG AAG GAT GAA TCC
asn val arg asp val ser pro phe pro val asn ala gly met thr val lys asp glu ser

FIG. 1 (cont.)

1502
CTG GCT CTA CCA GCT GTG AAT CCG CTG GTG ACG CCG CAG AAG GGA AGC ACC CTG GAC AAC
leu ala leu pro ala val asn pro leu val thr pro gln lys gly ser thr leu asp asn

1532
1562
AGC CTG CAC AAG GAC CTG CTG GGC GCC ATC TCC GGC ATT GCT TCT CCA TAT ACA ACC TCA
ser leu his lys asp leu leu gly ala ile ser gly ile ala ser pro tyr thr thr ser

1592
1622
ACT CCA AAC ATC AAC AGT GTG AGA AAT GCT GAT TCG AGA GGA TCT CTC ATA AGC ACA GAT
thr pro asn ile asn ser val arg asn ala asp ser arg gly ser leu ile ser thr asp

1652
1682
TCG GGT AAC AGC CTT CCA GAA AGG AAT AGT GAG AAG AGC AAT TCC CTG GAT AAG CAC CAA
ser gly asn ser leu pro glu arg asn ser glu lys ser asn ser leu asp lys his gln

1712
1742
CAA AGT AGC ACA TTG GGA AAT TCC GTG GTT CGC TGT GAT AAA CTT GAC CAG TCT GAG ATT
gln ser ser thr leu gly asn ser val val arg cys asp lys leu asp gln ser glu ile

1772
1802
AAG AGC CTA CTG ATG TGT TTC CTC TAC ATC TTA AAG AGC ATG TCT GAT GAT GCT TTG TTT
lys ser leu leu met cys phe leu tyr ile leu lys ser met ser asp asp ala leu phe

1832
1862
ACA TAT TGG AAC AAG GCT TCA ACA TCT GAA CTT ATG GAT TTT TTT ACA ATA TCT GAA GTC
thr tyr trp asn lys ala ser thr ser glu leu met asp phe phe thr ile ser glu val

1892
1922
TGC CTG CAC CAG TTC CAG TAC ATG GGG AAG CGA TAC ATA GCC AGG AAC CAG GAG GGG TTG
cys leu his gln phe gln tyr met gly lys arg tyr ile ala arg asn gln glu gly leu

1952
1982
GGA CCC ATA GTT CAT GAT CGA AAG TCT CAG ACA TTG CCT GTT TCC CGT AAC AGA ACA GGA
gly pro ile val his asp arg lys ser gln thr leu pro val ser arg asn arg thr gly

2012
2042
ATG ATG CAT GCC AGA TTG CAG CAG CTG GGC AGC CTG GAT AAC TCT CTC ACT TTT AAC CAC
met met his ala arg leu gln gln leu gly ser leu asp asn ser leu thr phe asn his

2072
2102
AGC TAT GGC CAC TCG GAC GCA GAT GTT CTG CAC CAG TCA TTA CTT GAA GCC AAC ATT GCT
ser tyr gly his ser asp ala asp val leu his gln ser leu leu glu ala asn ile ala

2132
2162
ACT GAG GTT TGC CTG ACA GCT CTG GAC ACG CTT TCT CTA TTT ACA TTG GCG TTT AAG AAC
thr glu val cys leu thr ala leu asp thr leu ser leu phe thr leu ala phe lys asn

2192
2222
CAG CTC CTG GCC GAC CAT GGA CAT AAT CCT CTC ATG AAA AAA GTT TTT GAT GTC TAC CTG
gln leu leu ala asp his gly his asn pro leu met lys lys val phe asp val tyr leu

2252

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2282                                2312
TGT TTT CTT CAA AAA CAT CAG TCT GAA ACG GCT TTA AAA AAT GTC TTC ACT GCC TTA AGG
cys phe leu gln lys his gln ser glu thr ala leu lys asn val phe thr ala leu arg

2342                                2372
TCC TTA ATT TAT AAG TTT CCC TCA ACA TTC TAT GAA GGG AGA GCG GAC ATG TGT GCG GCT
ser leu ile tyr lys phe pro ser thr phe tyr glu gly arg ala asp met cys ala ala

2402                                2432
CTG TGT TAC GAG ATT CTC AAG TGC TGT AAC TCC AAG CTG AGC TCC ATC AGG ACG GAG GCC
leu cys tyr glu ile leu lys cys cys asn ser lys leu ser ser ile arg thr glu ala

2462                                2492
TCC CAG CTG CTC TAC TTC CTG ATG AGG AAC AAC TTT GAT TAC ACT GGA AAG AAG TCC TTT
ser gln leu leu tyr phe leu met arg asn asn phe asp tyr thr gly lys lys ser phe

2522                                2552
GTC CGG ACA CAT TTG CAA GTC ATC ATA TCT GTC AGC CAG CTG ATA GCA GAC GTT GTT GGC
val arg thr his leu gln val ile ile ser val ser gln leu ile ala asp val val gly

2582                                2612
ATT GGG GAA ACC AGA TTC CAG CAG TCC CTG TCC ATC ATC AAC AAC TGT GCC AAC AGT GAC
ile gly glu thr arg phe gln gln ser leu ser ile ile asn asn cys ala asn ser asp

2642                                2672
CGG CTT ATT AAG CAC ACC AGC TTC TCC TCT GAT GTG AAG GAC TTA ACC AAA AGG ATA CGC
arg leu ile lys his thr ser phe ser ser asp val lys asp leu thr lys arg ile arg

2702                                2732
ACG GTG CTA ATG GCC ACC GCC CAG ATG AAG GAG CAT GAG AAC GAC CCA GAG ATG CTG GTG
thr val leu met ala thr ala gln met lys glu his glu asn asp pro glu met leu val

2762                                2792
GAC CTC CAG TAC AGC CTG GCC AAA TCC TAT GCC AGC ACG CCC GAG CTC AGG AAG ACG TGG
asp leu gln tyr ser leu ala lys ser tyr ala ser thr pro glu leu arg lys thr trp

2822                                2852                                |XXXXXXXXXXXXXXXXXXXX Predicted
CTC GAC AGC ATG GCC AGG ATC CAT GTC AAA AAT GGC GAT CTC TCA GAG GCA GCA ATG TGC
leu asp ser met ala arg ile his val lys asn gly asp leu ser glu ala ala met cys

Transmembrane Domain XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX|
TAT GTC CAC GTA ACA GCC CTA GTG GCA GAA TAT CTC ACA CGG AAA GGC GTG TTT AGA CAA
tyr val his val thr ala leu val ala glu tyr leu thr arg lys gly val phe arg gln

2942                                2972
GGA TGC ACC GCC TTC AGG GTC ATT ACC CCA AAC ATC GAC GAG GAG GCC TCC ATG ATG GAA
gly cys thr ala phe arg val ile thr pro asn ile asp glu glu ala ser met met glu

3002                                3032
GAC GTG GGG ATG CAG GAT GTC CAT TTC AAC GAG GAT GTG CTG ATG GAG CTC CTT GAG CAG
asp val gly met gln asp val his phe asn glu asp val leu met glu leu leu glu gln

3062                                3092
TGC GCA GAT GGA CTC TGG AAA GCC GAG CGC TAC GAG CTC ATC GCC GAC ATC TAC AAA CTT
cys ala asp gly leu trp lys ala glu arg tyr glu leu ile ala asp ile tyr lys leu

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FIG. 1 (cont.)

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3122                                     3155
ATC ATC CCC ATT TAT GAG AAG CGG AGG GAT TTC TTT GAA GAT GAA GAT GGA AAG GAG TAT
ile ile pro ile tyr glu lys arg arg asp phe phe glu asp glu asp gly lys glu tyr

3182                                     3212
ATT TAC AAG GAA CCC AAA CTC ACA CCG CTG TCG GAA ATT TCT CAG AGA CTC CTT AAA CTG
ile tyr lys glu pro lys leu thr pro leu ser glu ile ser gln arg leu leu lys leu

3242                                     3272
TAC TCG GAT AAA TTT GGT TCT GAA AAT GTC AAA ATG ATA CAG GAT TCT GGC AAG GTC AAC
tyr ser asp lys phe gly ser glu asn val lys met ile gln asp ser gly lys val asn

3302                                     3332
CCT AAG GAT CTG GAT TCT AAG TAT GCA TAC ATC CAG GTG ACT CAC GTC ATC CCC TTC TTT
pro lys asp leu asp ser lys tyr ala tyr ile gln val thr his val ile pro phe phe

3362                                     3392
GAC GAA AAA GAG TTG CAA GAA AGG AAA ACA GAG TTT GAG AGA TCC CAC AAC ATC CGC CGC
asp glu lys glu leu gln glu arg lys thr glu phe glu arg ser his asn ile arg arg

3422                                     3452
TTC ATG TTT GAG ATG CCA TTT ACG CAG ACC GGG AAG AGG CAG GGC GGG GTG GAA GAG CAG
phe met phe glu met pro phe thr gln thr gly lys arg gln gly gly val glu glu gln

3482                                     3512
TGC AAA CGG CGC ACC ATC CTG ACA GCC ATA CAC TGC TTC CCT TAT GTG AAG AAG CGC ATC
cys lys arg arg thr ile leu thr ala ile his cys phe pro tyr val lys lys arg ile

3542                                     3572 |XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
CCT GTC ATG TAC CAG CAC CAC ACT GAC CTG AAC CCC ATC GAG GTG GCC ATT GAC GAG ATG
pro val met tyr gln his his thr asp leu asn pro ile glu val ala ile asp glu met

3602 xxx Coiled-Coil 1 XXXXXXXXXXXXXXXX 3632 xxx Coiled-Coil 1 XXXXXXXXXXXXXXXX
AGT AAG AAG GTG GCG GAG CTC CGG CAG CTG TGC TCC TCG GCC GAG GTG GAC ATG ATC AAA
ser lys lys val ala glu leu arg gln leu cys ser ser ala glu val asp met ile lys

3662 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX | 3692
CTG CAG CTC AAA CTC CAG GGC AGC GTG AGT GTT CAG GTC AAT GCT GGC CCA CTA GCA TAT
leu gln leu lys leu gln gly ser val ser val gln val asn ala gly pro leu ala tyr

3722                                     3752
GCG CGA GCT TTC TTA GAT GAT ACA AAC ACA AAG CGA TAT CCT GAC AAT AAA GTG AAG CTG
ala arg ala phe leu asp asp thr asn thr lys arg tyr pro asp asn lys val lys leu

3782                                     3812 |XXXXXXXXXXXXXXXXXXXXXXXXXXXX
CTT AAG GAA GTT TTC AGG CAA TTT GTG GAA GCT TGC GGT CAA GCC TTA GCG GTA AAC GAA
leu lys glu val phe arg gln phe val glu ala cys gly gln ala leu ala val asn glu

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FIG. 1 (cont.)

3842 ~~xxx~~ Coiled-Coil 2 ~~xxxxxxxxxxxxxxxx~~ 3872 ~~xx~~
CGT CTG ATT AAA GAA GAC CAG CTC GAG TAT CAG GAA GAA ATG AAA GCC AAC TAC AGG GAA
arg leu ile lys glu asp gln leu glu tyr gln glu glu met lys ala asn tyr arg glu

3902 ~~xxx~~ Coiled-Coil 2 ~~xxxxxxxxxxxxxxxx~~ 3932 ~~xxxxxx~~
ATG GCG AAG GAG CTT TCT GAA ATC ATG CAT GAG CAG ATC TGC CCC CTG GAG GAG AAG ACG
met ala lys glu leu ser glu ile met his glu gln ile cys pro leu glu glu lys thr

3962 3992
AGC GTC TTA CCG AAT TCC CTT CAC ATC TTC AAC GCC ATC AGT GGG ACT CCA ACA AGC ACA
ser val leu pro asn ser leu his ile phe asn ala ile ser gly thr pro thr ser thr

4022 ~~xxxxx~~ PBM ~~xxxxx~~
ATG GTT CAC GGG ATG ACC AGC TCG TCT TCG GTC GTG TGA TTA CAT CTC ATG GCC CGT GTG
met val his gly met thr ser ser ser ser val val STP

4082 4112
TGG GGA CTT GCT TTG TCA TTT GCA AAC TCA GGA TGC TTT CCA AAG CCA ATC ACT GGG GAG

4142 4172
ACC GAG CAC AAG GAG GAC CAA GGG GAA GGG GAG AGA AAG GAA ATA AAG AAC AAC GTT ATT

4202 4232
TCT TAA CAG ACT TTC TAT AGG AGT TGT AAG AAG GTG CAC ATA TTT TTT TAA ATC TCA CTG

4262 4292
GCA ATA TTC AAA GTT TTC ATT GTG TCT TAA CAA AGG TGT GGT AGA CAC TCT TGA GCT GGA

4322 4352
CTT AGA TTT TAT TCT TCC TTG CAG AGT AGT GTT AGA ATA GAT GGC CTA CAG AAA AAA AAG

4382 4412
GTT CTG GGA TCT ACA TGG CAG GGA GGG CTG CAC TGA CAT TGA TGC CTG GGG GAC CTT TTG

4442 4472
CCT CGA CTC GTG CCG GAA ATC TGA TCG TAA TCA GGG TAC AGA ACT TAC TAG TTT TGT CTA

4502 4532
GGA GTA TGT TGT ATG ACT AGG ATT TGT GCT ATT ATC TCA TTC AAC AAC ATA GAG CAA GAA

4562 4592
TAG TGA GCT AAC TGA GCT AGA CAC TCA ATT AAT CCG CTA CTG GCT TCA AGT CAG AAC TTT

4622 4652
GTC ATT AAT CAT CGA CTC CGG GAC GGT CAT ATA TGT ATT ACA TTT CTA CAT TTT TAA TAC

4682 4712
TCA CAT GGG CTT ATG CAT TAA GTT TAA TTG TGA TAA ATT TGT GCT GGT CCA GTA TAT GCA

4742 4772
ATA CAC TTT AAT GGT TTA TTC TTG TCA TAA AAA TGT GCA ATA TGG AGA TGT ATA CAA GTC

4802
TTT ACT

FIG. 1 (cont.)

(Nucleotide position for insertions and deletions are found above the Human (h) CLASP-2A line diagram. Numbers are referenced based on hCLASP-2A nucleotide sequence from Figure 1.)

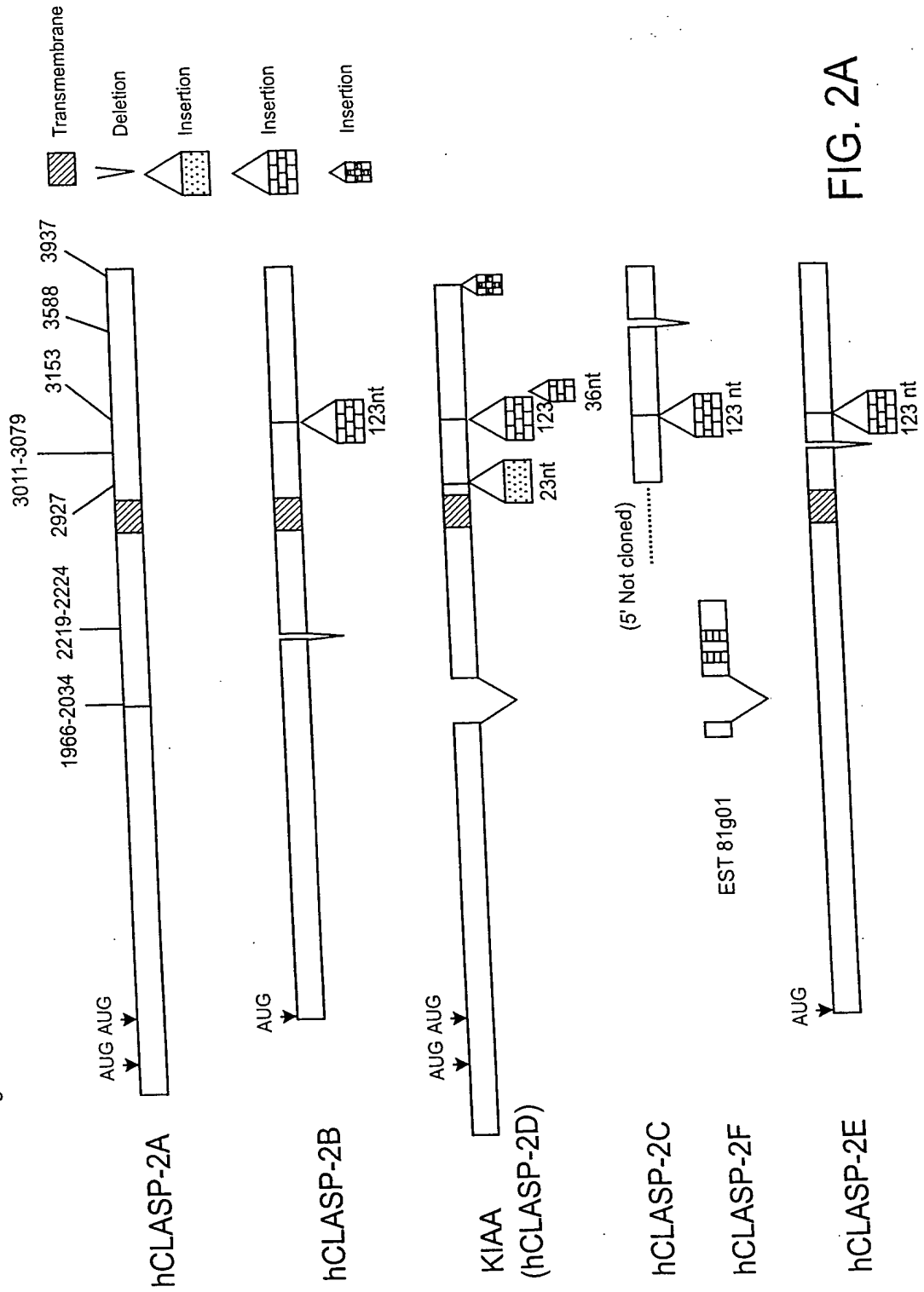


FIG. 2A

2
 GTT TTA CAC CAT CAC CAA AAC CCA GAA TTT TAT GAT GAG ATT AAA ATA GAG TTG CCC ACT
 val leu his his his gln asn pro glu phe tyr asp glu ile lys ile glu leu pro thr

62
 CAG CTG CAT GAA AAG CAC CAC CTG TTG CTC ACA TTC TTC CAT GTC AGC TGT GAC AAC TCA
 gln leu his glu lys his his leu leu leu thr phe phe his val ser cys asp asn ser

122
 AGT AAA GGA AGC ACG AAG AAG AGG GAT GTC GTT GAA ACC CAA GTT GGC TAC TCC TGG CTT
 ser lys gly ser thr lys lys arg asp val val glu thr gln val gly tyr ser trp leu

182
 CCC CTC CTG AAA GAC GGA AGG GTG GTG ACA AGC GAG CAG CAC ATC CCG GTC TCG GCG AAC
 pro leu leu lys asp gly arg val val thr ser glu gln his ile pro val ser ala asn

242
 CTT CCT TCG GGC TAT CTT GGC TAC CAA GAG CTT GGG ATG GGC AGG CAT TAT GGT CCG GAA
 leu pro ser gly tyr leu gly tyr gln glu leu gly met gly arg his tyr gly pro glu

302
 ATT AAA TGG GTA GAT GGA GGC AAG CCA CTG CTG AAA ATT TCC ACT CAT CTG GTT TCT ACA
 ile lys trp val asp gly gly lys pro leu leu lys ile ser thr his leu val ser thr

362
 GTG TAT ACT CAG GAT CAG CAT TTA CAT AAT TTT TTC CAG TAC TGT CAG AAA ACC GAA TCT
 val tyr thr gln asp gln his leu his asn phe phe gln tyr cys gln lys thr glu ser

422
 GGA GCC CAA GCC TTA GGA AAC GAA CTT GTA AAG TAC CTT AAG AGT CTG CAT GCG ATG GAA
 gly ala gln ala leu gly asn glu leu val lys tyr leu lys ser leu his ala met glu

482
 GGC CAC GTG ATG ATC GCC TTC TTG CCC ACT ATC CTA AAC CAG CTG TTC CGA GTC CTC ACC
 gly his val met ile ala phe leu pro thr ile leu asn gln leu phe arg val leu thr

542
 AGA GCC ACA CAG GAA GAA GTC GCG GTT AAC GTG ACT CGG GTC ATT ATT CAT GTG GTT GCC
 arg ala thr gln glu glu val ala val asn val thr arg val ile ile his val val ala

602
 CAG TGC CAT GAG GAA GGA TTG GAG AGC CAC TTG AGG TCA TAT GTT AAG TAC GCG TAT AAG
 gln cys his glu glu gly leu glu ser his leu arg ser tyr val lys tyr ala tyr lys

662
 GCT GAG CCA TAT GTT GCC TCT GAA TAC AAG ACA GTG CAT GAA GAA CTG ACC AAA TCC ATG
 ala glu pro tyr val ala ser glu tyr lys thr val his glu glu leu thr lys ser met

FIG. 2B

722
 ACC ACG ATT CTC AAG CCT TCT GCC GAT TTC CTC ACC AGC AAC AAA CTA CTG AGG TAC TCA
 thr thr ile leu lys pro ser ala asp phe leu thr ser asn lys leu leu arg tyr ser

752
 782
 TGG TTT TTC TTT GAT GTA CTG ATC AAA TCT ATG GCT CAG CAT TTG ATA GAG AAC TCC AAA
 trp phe phe phe asp val leu ile lys ser met ala gln his leu ile glu asn ser lys

812
 842 |Cadherin Cleavage| 872
 GTT AAG TTG CTG CGA AAC CAG AGA TTT CCT GCA TCC TAT CAT CAT GCA GCG GAA ACC GTT
 val lys leu leu arg asn gln arg phe pro ala ser tyr his his ala ala glu thr val

902
 932
 GTA AAT ATG CTG ATG CCA CAC ATC ACT CAG AAG TTT GGA GAT AAT CCA GAG GCA TCT AAG
 val asn met leu met pro his ile thr gln lys phe gly asp asn pro glu ala ser lys

962
 992
 AAC GCG AAT CAT AGC CTT GCT GTC TTC ATC AAG AGA TGT TTC ACC TTC ATG GAC AGG GGC
 asn ala asn his ser leu ala val phe ile lys arg cys phe thr phe met asp arg gly

1022
 1052
 TTT GTC TTC AAG CAG ATC AAC AAC TAC ATT AGC TGT TTT GCT CCT GGA GAC CCA AAG ACC
 phe val phe lys gln ile asn asn tyr ile ser cys phe ala pro gly asp pro lys thr

1082
 1112
 CTC TTT GAA TAC AAG TTT GAA TTT CTC CGT GTA GTG TGC AAC CAT GAA CAT TAT ATT CCG
 leu phe glu tyr lys phe glu phe leu arg val val cys asn his glu his tyr ile pro

1142
 1172
 TTG AAC TTA CCA ATG CCA TTT GGA AAA GGC AGG ATT CAA AGA TAC CAA GAC CTC CAG CTT
 leu asn leu pro met pro phe gly lys gly arg ile gln arg tyr gln asp leu gln leu

1202
 1232 |Cadherin EC
 GAC TAC TCA TTA ACA GAT GAG TTC TGC AGA AAC CAC TTC TTG GTG GGA CTG TTA CTG AGG
 asp tyr ser leu thr asp glu phe cys arg asn his phe leu val gly leu leu leu arg

1292
 xxx|
 GAG GTG GGG ACA GCC CTC CAG GAG TTC CGG GAG GTC CGT CTG ATC GCC ATC AGT GTG CTC
 glu val gly thr ala leu gln glu phe arg glu val arg leu ile ala ile ser val leu

1322
 1352
 AAG AAC CTG CTG ATA AAG CAT TCT TTT GAT GAC AGA TAT GCT TCA AGG AGC CAT CAG GCA
 lys asn leu leu ile lys his ser phe asp asp arg tyr ala ser arg ser his gln ala

1382
 1412
 AGG ATA GCC ACC CTC TAC CTG CCT CTG TTT GGT CTG CTG ATT GAA AAC GTC CAG CGG ATC
 arg ile ala thr leu tyr leu pro leu phe gly leu leu ile glu asn val gln arg ile

1442
 1472
 AAT GTG AGG GAT GTG TCA CCC TTC CCT GTG AAC GCG GGC ATG ACC GTG AAG GAT GAA TCC
 asn val arg asp val ser pro phe pro val asn ala gly met thr val lys asp glu ser

FIG. 2B (cont.)

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1502                                1532
CTG GCT CTA CCA GCT GTG AAT CCG CTG GTG ACG CCG CAG AAG GGA AGC ACC CTG GAC AAC
leu ala leu pro ala val asn pro leu val thr pro gln lys gly ser thr leu asp asn

1562                                1592
AGC CTG CAC AAG GAC CTG CTG GGC GCC ATC TCC GGC ATT GCT TCT CCA TAT ACA ACC TCA
ser leu his lys asp leu leu gly ala ile ser gly ile ala ser pro tyr thr thr ser

1622                                1652
ACT CCA AAC ATC AAC AGT GTG AGA AAT GCT GAT TCG AGA GGA TCT CTC ATA AGC ACA GAT
thr pro asn ile asn ser val arg asn ala asp ser arg gly ser leu ile ser thr asp

1682                                1712
TCG GGT AAC AGC CTT CCA GAA AGG AAT AGT GAG AAG AGC AAT TCC CTG GAT AAG CAC CAA
ser gly asn ser leu pro glu arg asn ser glu lys ser asn ser leu asp lys his gln

1742                                1772
CAA AGT AGC ACA TTG GGA AAT TCC GTG GTT CGC TGT GAT AAA CTT GAC CAG TCT GAG ATT
gln ser ser thr leu gly asn ser val val arg cys asp lys leu asp gln ser glu ile

1802                                1832
AAG AGC CTA CTG ATG TGT TTC CTC TAC ATC TTA AAG AGC ATG TCT GAT GAT GCT TTG TTT
lys ser leu leu met cys phe leu tyr ile leu lys ser met ser asp asp ala leu phe

1862                                1892
ACA TAT TGG AAC AAG GCT TCA ACA TCT GAA CTT ATG GAT TTT TTT ACA ATA TCT GAA GTC
thr tyr trp asn lys ala ser thr ser glu leu met asp phe phe thr ile ser glu val

1922                                1952
TGC CTG CAC CAG TTC CAG TAC ATG GGG AAG CGA TAC ATA GCC AGG AAC CAG GAG GGG TTG
cys leu his gln phe gln tyr met gly lys arg tyr ile ala arg asn gln glu gly leu

1982 xxxxxxxxxxxx deleted in CLASP-2D(KIAA1058) xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx|
GGA CCC ATA GTT CAT GAT CGA AAG TCT CAG ACA TTG CCT GTT TCC CGT AAC AGA ACA GGA
gly pro ile val his asp arg lys ser gln thr leu pro val ser arg asn arg thr gly

2042                                2072
ATG ATG CAT GCC AGA TTG CAG CAG CTG GGC AGC CTG GAT AAC TCT CTC ACT TTT AAC CAC
met met his ala arg leu gln gln leu gly ser leu asp asn ser leu thr phe asn his

2102                                2132
AGC TAT GGC CAC TCG GAC GCA GAT GTT CTG CAC CAG TCA TTA CTT GAA GCC AAC ATT GCT
ser tyr gly his ser asp ala asp val leu his gln ser leu leu glu ala asn ile ala

2162                                2192
ACT GAG GTT TGC CTG ACA GCT CTG GAC ACG CTT TCT CTA TTT ACA TTG GCG TTT AAG AAC
thr glu val cys leu thr ala leu asp thr leu ser leu phe thr leu ala phe lys asn

in HC2B
xxx|
CAG CTC CTG GCC GAC CAT GGA CAT AAT CCT CTC ATG AAA AAA GTT TTT GAT GTC TAC CTG
gln leu leu ala asp his gly his asn pro leu met lys lys val phe asp val tyr leu

```

Deleted
|xxx

FIG. 2B (cont.)

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2282
TGT TTT CTT CAA AAA CAT CAG TCT GAA ACG GCT TTA AAA AAT GTC TTC ACT GCC TTA AGG
cys phe leu gln lys his gln ser glu thr ala leu lys asn val phe thr ala leu arg

2312
2342
TCC TTA ATT TAT AAG TTT CCC TCA ACA TTC TAT GAA GGG AGA GCG GAC ATG TGT GCG GCT
ser leu ile tyr lys phe pro ser thr phe tyr glu gly arg ala asp met cys ala ala

2402
2432
CTG TGT TAC GAG ATT CTC AAG TGC TGT AAC TCC AAG CTG AGC TCC ATC AGG ACG GAG GCC
leu cys tyr glu ile leu lys cys cys asn ser lys leu ser ser ile arg thr glu ala

2462
2492
TCC CAG CTG CTC TAC TTC CTG ATG AGG AAC AAC TTT GAT TAC ACT GGA AAG AAG TCC TTT
ser gln leu leu tyr phe leu met arg asn asn phe asp tyr thr gly lys lys ser phe

2522
2552
GTC CGG ACA CAT TTG CAA GTC ATC ATA TCT GTC AGC CAG CTG ATA GCA GAC GTT GTT GGC
val arg thr his leu gln val ile ile ser val ser gln leu ile ala asp val val gly

2582
2612
ATT GGG GAA ACC AGA TTC CAG CAG TCC CTG TCC ATC ATC AAC AAC TGT GCC AAC AGT GAC
ile gly glu thr arg phe gln gln ser leu ser ile ile asn asn cys ala asn ser asp

2642
2672
CGG CTT ATT AAG CAC ACC AGC TTC TCC TCT GAT GTG AAG GAC TTA ACC AAA AGG ATA CGC
arg leu ile lys his thr ser phe ser ser asp val lys asp leu thr lys arg ile arg

2702
2732
ACG GTG CTA ATG GCC ACC GCC CAG ATG AAG GAG CAT GAG AAC GAC CCA GAG ATG CTG GTG
thr val leu met ala thr ala gln met lys glu his glu asn asp pro glu met leu val

2762
2792
GAC CTC CAG TAC AGC CTG GCC AAA TCC TAT GCC AGC ACG CCC GAG CTC AGG AAG ACG TGG
asp leu gln tyr ser leu ala lys ser tyr ala ser thr pro glu leu arg lys thr trp

2822
2852
CTC GAC AGC ATG GCC AGG ATC CAT GTC AAA AAT GGC GAT CTC TCA GAG GCA GCA ATG TGC
leu asp ser met ala arg ile his val lys asn gly asp leu ser glu ala ala met cys

[Additional and differential exon usage found at position 2927 consisting
of 69 nucleotides. This entire sequence is found in Human CLASP-2D
(KIAA1058) and not other isoforms of CLASP-2. It has a sequence of:
AAGCAGTCCAGTGGGAGCCGCCCTTCTCCCCACAGCCATAGCGCCTGCCTGAGGAGGAGCCGGGGAG]

Transmembrane Domain |XXXXXXXXXXXXXXXXXXXXXXXXXXXX|
TAT GTC CAC GTA ACA GCC CTA GTG GCA GAA TAT CTC ACA CGG AAA GGC GTG TTT AGA CAA
tyr val his val thr ala leu val ala glu tyr leu thr arg lys gly val phe arg gln

2942
2972
GGA TGC ACC GCC TTC AGG GTC ATT ACC CCA AAC ATC GAC GAG GAG GCC TCC ATG ATG GAA
gly cys thr ala phe arg val ile thr pro asn ile asp glu glu ala ser met met glu

FIG. 2B (cont.)

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3002 |xx Sequence deleted in CLASP-2E xxxxx
 GAC GTG GGG ATG CAG GAT GTC CAT TTC AAC GAG GAT GTG CTG ATG GAG CTC CTT GAG CAG
 asp val gly met gln asp val his phe asn glu asp val leu met glu leu leu glu gln

3062 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx 3092
 TGC GCA GAT GGA CTC TGG AAA GCC GAG CGC TAC GAG CTC ATC GCC GAC ATC TAC AAA CTT
 cys ala asp gly leu trp lys ala glu arg tyr glu leu ile ala asp ile tyr lys leu

[Additional and differential exon usage found at position 3153. The entire sequence below is found in Human CLASP-2D. Underlined sequence is found in Human CLASP-2B, 2C and 2E.

TGAGAGGCTGGCCCATCTGTATGACACGCTGCACCGGGCCTACAGCAAAGTGACCGAGGTCAT
GCACTCGGGCCGCGAGGCTTCTGGGGACCTACTCCGGGTAGCCTTCTTCGGGCAGGCAGCGCAATACCAGTTT
ACAGACAGTGAAACAGATGTGGAGGGATT]

3122 3155
 ATC ATC CCC ATT TAT GAG AAG CGG AGG GAT TTC TTT GAA GAT GAA GAT GGA AAG GAG TAT
 ile ile pro ile tyr glu lys arg arg asp phe phe glu asp glu asp gly lys glu tyr

3182 3212
 ATT TAC AAG GAA CCC AAA CTC ACA CCG CTG TCG GAA ATT TCT CAG AGA CTC CTT AAA CTG
 ile tyr lys glu pro lys leu thr pro leu ser glu ile ser gln arg leu leu lys leu

3242 3272
 TAC TCG GAT AAA TTT GGT TCT GAA AAT GTC AAA ATG ATA CAG GAT TCT GGC AAG GTC AAC
 tyr ser asp lys phe gly ser glu asn val lys met ile gln asp ser gly lys val asn

3302 3332
 CCT AAG GAT CTG GAT TCT AAG TAT GCA TAC ATC CAG GTG ACT CAC GTC ATC CCC TTC TTT
 pro lys asp leu asp ser lys tyr ala tyr ile gln val thr his val ile pro phe phe

3362 3392
 GAC GAA AAA GAG TTG CAA GAA AGG AAA ACA GAG TTT GAG AGA TCC CAC AAC ATC CGC CGC
 asp glu lys glu leu gln glu arg lys thr glu phe glu arg ser his asn ile arg arg

3422 3452
 TTC ATG TTT GAG ATG CCA TTT ACG CAG ACC GGG AAG AGG CAG GGC GGG GTG GAA GAG CAG
 phe met phe glu met pro phe thr gln thr gly lys arg gln gly gly val glu glu gln

3482 3512
 TGC AAA CGG CGC ACC ATC CTG ACA GCC ATA CAC TGC TTC CCT TAT GTG AAG AAG CGC ATC
 cys lys arg arg thr ile leu thr ala ile his cys phe pro tyr val lys lys arg ile

Two nucleotide deletion (nts 3586 and 3587) found in Human CLASP-2C

3542 3572 |xxx|
 CCT GTC ATG TAC CAG CAC CAC ACT GAC CTG AAC CCC ATC GAG GTG GCC ATT GAC GAG ATG
 pro val met tyr gln his his thr asp leu asn pro ile glu val ala ile asp glu met

FIG. 2B (cont.)

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3602 3632
AGT AAG AAG GTG GCG GAG CTC CGG CAG CTG TGC TCC TCG GCC GAG GTG GAC ATG ATC AAA
ser lys lys val ala glu leu arg gln leu cys ser ser ala glu val asp met ile lys

3662 3692
CTG CAG CTC AAA CTC CAG GGC AGC GTG AGT GTT CAG GTC AAT GCT GGC CCA CTA GCA TAT
leu gln leu lys leu gln gly ser val ser val gln val asn ala gly pro leu ala tyr

3722 3752
GCG CGA GCT TTC TTA GAT GAT ACA AAC ACA AAG CGA TAT CCT GAC AAT AAA GTG AAG CTG
ala arg ala phe leu asp asp thr asn thr lys arg tyr pro asp asn lys val lys leu

3782 3812
CTT AAG GAA GTT TTC AGG CAA TTT GTG GAA GCT TGC GGT CAA GCC TTA GCG GTA AAC GAA
leu lys glu val phe arg gln phe val glu ala cys gly gln ala leu ala val asn glu

3842 3872
CGT CTG ATT AAA GAA GAC CAG CTC GAG TAT CAG GAA GAA ATG AAA GCC AAC TAC AGG GAA
arg leu ile lys glu asp gln leu glu tyr gln glu glu met lys ala asn tyr arg glu

Insertion of 8 nucleotides found only in Human CLASP-2D with sequence: CTGGGATG

3902 3932
ATG GCG AAG GAG CTT TCT GAA ATC ATG CAT GAG CAG ATC TGC CCC CTG GAG GAG AAG ACG
met ala lys glu leu ser glu ile met his glu gln ile cys pro leu glu glu lys thr

3962 3992
AGC GTC TTA CCG AAT TCC CTT CAC ATC TTC AAC GCC ATC AGT GGG ACT CCA ACA AGC ACA
ser val leu pro asn ser leu his ile phe asn ala ile ser gly thr pro thr ser thr

4022 |XXXX PBM XXXX|
ATG GTT CAC GGG ATG ACC AGC TCG TCT TCG GTC GTG TGA TTA CAT CTC ATG GCC CGT GTG
met val his gly met thr ser ser ser val val STP

4082 4112
TGG GGA CTT GCT TTG TCA TTT GCA AAC TCA GGA TGC TTT CCA AAG CCA ATC ACT GGG GAG

4142 4172
ACC GAG CAC AGG GAG GAC CAA GGG GAA GGG GAG AGA AAG GAA ATA AAG AAC AAC GTT ATT

4202 4232
TCT TAA CAG ACT TTC TAT AGG AGT TGT AAG AAG GTG CAC ATA TTT TTT TAA ATC TCA CTG

4262 4292
GCA ATA TTC AAA GTT TTC ATT GTG TCT TAA CAA AGG TGT GGT AGA CAC TCT TGA GCT GGA

4322 4352
CTT AGA TTT TAT TCT TCC TTG CAG AGT AGT GTT AGA ATA GAT GGC CTA CAG AAA AAA AAG

4382 4412
GTT CTG GGA TCT ACA TGG CAG GGA GGG CTG CAC TGA CAT TGA TGC CTG GGG GAC CTT TTG

FIG. 2B (cont.)

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4442	4472
CCT CGA CTC GTG CCG GAA ATC TGA TCG TAA TCA GGG TAC AGA ACT TAC TAG TTT TGT CTA	
4502	4532
GGA GTA TGT TGT ATG ACT AGG ATT TGT GCT ATT ATC TCA TTC AAC AAC ATA GAG CAA GAA	
4562	4592
TAG TGA GCT AAC TGA GCT AGA CAC TCA ATT AAT CCG CTA CTG GCT TCA AGT CAG AAC TTT	
4622	4652
GTC ATT AAT CAT CGA CTC CGG GAC GGT CAT ATA TGT ATT ACA TTT CTA CAT TTT TAA TAC	
4682	4712
TCA CAT GGG CTT ATG CAT TAA GTT TAA TTG TGA TAA ATT TGT GCT GGT CCA GTA TAT GCA	
4742	4772
ATA CAC TTT AAT GGT TTA TTC TTG TCA TAA AAA TGT GCA ATA TGG AGA TGT ATA CAA GTC	
4802	
TTT ACT	

FIG. 2B (cont.)

HC2A
HC2-80
HC2B
HC2C
HC2D-KIAA1058
HC2E
HC2F

GCATCTGGAAATCTTGACAAAAATGCCAGATTTTCTGCCATCTACAGGCAAGACAGCAAT

HC2A
HC2-80
HC2B
HC2C
HC2D-KIAA1058
HC2E
HC2F

AAGCTATCCAATGATGACATGCTCAAGTTACTTGCAGACTTTCGGAAACCTGAGAAGATG

HC2A
HC2-80
HC2B
HC2C
HC2D-KIAA1058
HC2E
HC2F

GCTAAGCTCCCGAGTGATTTTAGGCAATCTAGACATTACAATTGATAATGTTTCCTCAGAC

HC2A
HC2-80
HC2B
HC2C
HC2D-KIAA1058
HC2E
HC2F

TTCCCTAATTATGTTAATTCATCATACATTCCCACAAAACAATTTGAAACCTGCAGTAAA

HC2A
HC2-80
HC2B
HC2C
HC2D-KIAA1058
HC2E
HC2F

ACTCCCATCACGTTTGAAGTGGAGGAATTTGTGCCCTGCATACCAAAACACACTCAGCCT

FIG. 3A

HC2A -----
 HC2-80 -----
 HC2B -----
 HC2C -----
 HC2D-KIAA1058 TACACCATCTACACCAATCACCTTTACGTTTATCCTAAGTACTTGAAATACGACAGTCAG
 HC2E -----
 HC2F -----

HC2A -----
 HC2-80 -----
 HC2B -----
 HC2C -----
 HC2D-KIAA1058 AAGTCTTTTGCCAAGGCTAGAAATATTGCGATTGTCATTGAATTCAAAGATTCAGATGAG
 HC2E -----
 HC2F -----

HC2A -----
 HC2-80 -----
 HC2B -----
 HC2C -----
 HC2D-KIAA1058 GAAGACTCTCAGCCCCCTTAAGTGCATTTATGGCAGACCTGGTGGGCCAGTTTTCACAAGA
 HC2E -----
 HC2F -----

HC2A -----AGTTTACACCATCACCAAACCCAGAATTTTATGATGAGATTAAA
 HC2-80 -----
 HC2B -----
 HC2C -----
 HC2D-KIAA1058 AGCGCCTTTGCTGCAGTTTACACCATCACCAAACCCAGAATTTTATGATGAGATTAAA
 HC2E -----
 HC2F -----

HC2A ATAGAGTTGCCCACTCAGCTGCATGAAAAGCACCACTGTTGCTCACATTCTTCCATGTC
 HC2-80 -----
 HC2B -----
 HC2C -----
 HC2D-KIAA1058 ATAGAGTTGCCCACTCAGCTGCATGAAAAGCACCACTGTTGCTCACATTCTTCCATGTC
 HC2E -----
 HC2F -----

HC2A AGCTGTGACAACTCAAGTAAAGGAAGCACGAAGAAGAGGGATGTCGTTGAAACCCAAGTT
 HC2-80 -----
 HC2B -----
 HC2C -----
 HC2D-KIAA1058 AGCTGTGACAACTCAAGTAAAGGAAGCACGAAGAAGAGGGATGTCGTTGAAACCCAAGTT
 HC2E -----
 HC2F -----

FIG. 3A (cont.)

HC2A	GGCTACTCCTGGCTTCCCCCTCCTGAAAGACGGAAGGGTGGTGACAAGCGAGCAGCACATC
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	GGCTACTCCTGGCTTCCCCCTCCTGAAAGACGGAAGGGTGGTGACAAGCGAGCAGCACATC
HC2E	-----
HC2F	-----

HC2A	CCGGTCTCGGCGAACCTTCCTTCGGGCTATCTTGGCTACCAAGAGCTTGGGATGGGCAGG
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	CCGGTCTCGGCGAACCTTCCTTCGGGCTATCTTGGCTACCAAGAGCTTGGGATGGGCAGG
HC2E	-----
HC2F	-----

HC2A	CATTATGGTCCGGAAATTAAATGGGTAGATGGAGGCAAGCCACTGCTGAAAATTTCCACT
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	CATTATGGTCCGGAAATTAAATGGGTAGATGGAGGCAAGCCACTGCTGAAAATTTCCACT
HC2E	-----
HC2F	-----

HC2A	CATCTGGTTTCTACAGTGTATACTCAGGATCAGCATTTACATAATTTTTTCCAGTACTGT
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	CATCTGGTTTCTACAGTGTATACTCAGGATCAGCATTTACATAATTTTTTCCAGTACTGT
HC2E	-----
HC2F	-----

HC2A	CAGAAAACCGAATCTGGAGCCCAAGCCTTAGGAAACGAACTTGTAAGTACCTTAAGAGT
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	CAGAAAACCGAATCTGGAGCCCAAGCCTTAGGAAACGAACTTGTAAGTACCTTAAGAGT
HC2E	-----
HC2F	-----

HC2A	CTGCATGCGATGGAAGGCCACGTGATGATCGCCTTCTTGCCCACTATCCTAAACCAGCTG
HC2-80	-----
HC2B	-----GCGATGGAAGGCCACGTGATGATCGCCTTCTTGCCCACTATCCTAAACCAGCTG
HC2C	-----
HC2D-KIAA1058	CTGCATGCGATGGAAGGCCACGTGATGATCGCCTTCTTGCCCACTATCCTAAACCAGCTG
HC2E	-----GCGATGGAAGGCCACGTGATGATCGCCTTCTTGCCCACTATCCTAAACCAGCTG
HC2F	-----

FIG. 3A (cont.)

HC2A	TTCCGAGTCCTCACCAGAGCCACACAGGAAGAAGTCGCGGTTAACGTGACTCGGGTCATT
HC2-80	-----
HC2B	TTCCGAGTCCTCACCAGAGCCACACAGGAAGAAGTCGCGGTTAACGTGACTCGGGTCATT
HC2C	-----
HC2D-KIAA1058	TTCCGAGTCCTCACCAGAGCCACACAGGAAGAAGTCGCGGTTAACGTGACTCGGGTCATT
HC2E	TTCCGAGTCCTCACCAGAGCCACACAGGAAGAAGTCGCGGTTAACGTGACTCGGGTCATT
HC2F	-----
HC2A	ATTCATGTGGTTGCCCAGTGCCATGAGGAAGGATTGGAGAGCCACTTGAGGTCATATGTT
HC2-80	-----
HC2B	ATTCATGTGGTTGCCCAGTGCCATGAGGAAGGATTGGAGAGCCACTTGAGGTCATATGTT
HC2C	-----
HC2D-KIAA1058	ATTCATGTGGTTGCCCAGTGCCATGAGGAAGGATTGGAGAGCCACTTGAGGTCATATGTT
HC2E	ATTCATGTGGTTGCCCAGTGCCATGAGGAAGGATTGGAGAGCCACTTGAGGTCATATGTT
HC2F	-----
HC2A	AAGTACGCGTATAAGGCTGAGCCATATGTTGCCTCTGAATACAAGACAGTGCATGAAGAA
HC2-80	-----
HC2B	AAGTACGCGTATAAGGCTGAGCCATATGTTGCCTCTGAATACAAGACAGTGCATGAAGAA
HC2C	-----
HC2D-KIAA1058	AAGTACGCGTATAAGGCTGAGCCATATGTTGCCTCTGAATACAAGACAGTGCATGAAGAA
HC2E	AAGTACGCGTATAAGGCTGAGCCATATGTTGCCTCTGAATACAAGACAGTGCATGAAGAA
HC2F	-----
HC2A	CTGACCAAATCCATGACCACGATTCTCAAGCCTTCTGCCGATTTCCCTCACCAGCAACAAA
HC2-80	-----
HC2B	CTGACCAAATCCATGACCACGATTCTCAAGCCTTCTGCCGATTTCCCTCACCAGCAACAAA
HC2C	-----
HC2D-KIAA1058	CTGACCAAATCCATGACCACGATTCTCAAGCCTTCTGCCGATTTCCCTCACCAGCAACAAA
HC2E	CTGACCAAATCCATGACCACGATTCTCAAGCCTTCTGCCGATTTCCCTCACCAGCAACAAA
HC2F	-----
HC2A	CTACTGAGGTACTCATGGTTTTTCTTTGATGTACTGATCAAATCTATGGCTCAGCATTTG
HC2-80	-----
HC2B	CTACTGAGGTACTCATGGTTTTTCTTTGATGTACTGATCAAATCTATGGCTCAGCATTTG
HC2C	-----
HC2D-KIAA1058	CTACTGAAGTACTCATGGTTTTTCTTTGATGTACTGATCAAATCTATGGCTCAGCATTTG
HC2E	CTACTGAGGTACTCATGGTTTTTCTTTGATGTACTGATCAAATCTATGGCTCAGCATTTG
HC2F	-----
HC2A	ATAGAGAACTCCAAAGTTAAGTTGCTGCGAAACCAGAGATTTCCCTGCATCCTATCATCAT
HC2-80	-----
HC2B	ATAGAGAACTCCAAAGTTAAGTTGCTGCGAAACCAGAGATTTCCCTGCATCCTATCATCAT
HC2C	-----
HC2D-KIAA1058	ATAGAGAACTCCAAAGTTAAGTTGCTGCGAAACCAGAGATTTCCCTGCATCCTATCATCAT
HC2E	ATAGAGAACTCCAAAGTTAAGTTGCTGCGAAACCAGAGATTTCCCTGCATCCTATCATCAT
HC2F	-----

FIG. 3A (cont.)

HC2A	GCAGCGGAAACCGTTGTAAATATGCTGATGCCACACATCACTCAGAAGTTTGGAGATAAT
HC2-80	-----
HC2B	GCAGCGGAAACCGTTGTAAATATGCTGATGCCACACATCACTCAGAAGTTTGGAGATAAT
HC2C	-----
HC2D-KIAA1058	GCAGTGGAAACCGTTGTAAATATGCTGATGCCACACATCACTCAGAAGTTTGGAGATAAT
HC2E	GCAGCGGAAACCGTTGTAAATATGCTGATGCCACACATCACTCAGAAGTTTGGAGATAAT
HC2F	-----
HC2A	CCAGAGGCATCTAAGAACGCGAATCATAGCCTTGCTGTCTTCATCAAGAGATGTTTCACC
HC2-80	-----
HC2B	CCAGAGGCATCTAAGAACGCGAATCATAGCCTTGCTGTCTTCATCAAGAGATGTTTCACC
HC2C	-----
HC2D-KIAA1058	CCAGAGGCATCTAAGAACGCGAATCATAGCCTTGCTGTCTTCATCAAGAGATGTTTCACC
HC2E	CCAGAGGCATCTAAGAACGCGAATCATAGCCTTGCTGTCTTCATCAAGAGATGTTTCACC
HC2F	-----
HC2A	TTCATGGACAGGGGCTTTGTCTTCAAGCAGATCAACAACCTACATTAGCTGTTTTGCTCCT
HC2-80	-----
HC2B	TTCATGGACAGGGGCTTTGTCTTCAAGCAGATCAACAACCTACATTAGCTGTTTTGCTCCT
HC2C	-----
HC2D-KIAA1058	TTCATGGACAGGGGCTTTGTCTTCAAGCAGATCAACAACCTACATTAGCTGTTTTGCTCCT
HC2E	TTCATGGACAGGGGCTTTGTCTTCAAGCAGATCAACAACCTACATTAGCTGTTTTGCTCCT
HC2F	-----
HC2A	GGAGACCCAAAGACCCTCTTTGAATACAAGTTTGAATTTCTCCGTGTAGTGTGCAACCAT
HC2-80	-----
HC2B	GGAGACCCAAAGACCCTCTTTGAATACAAGTTTGAATTTCTCCGTGTAGTGTGCAACCAT
HC2C	-----
HC2D-KIAA1058	GGAGACCCAAAGACCCTCTTTGAATACAAGTTTGAATTTCTCCGTGTAGTGTGCAACCAT
HC2E	GGAGACCCAAAGACCCTCTTTGAATACAAGTTTGAATTTCTCCGTGTAGTGTGCAACCAT
HC2F	-----
HC2A	GAACATTATATTCCGTTGAACTTACCAATGCCATTTGGAAAAGGCAGGATTCAAAGATAC
HC2-80	-----
HC2B	GAACATTATATTCCGTTGAACTTACCAATGCCATTTGGAAAAGGCAGGATTCAAAGATAC
HC2C	-----
HC2D-KIAA1058	GAACATTATATTCCGTTGAACTTACCAATGCCATTTGGAAAAGGCAGGATTCAAAGATAC
HC2E	GAACATTATATTCCGTTGAACTTACCAATGCCATTTGGAAAAGGCAGGATTCAAAGATAC
HC2F	-----
HC2A	CAAGACCTCCAGCTTGACTACTCATTAAACAGATGAGTTCTGCAGAAACCACTTCTTGGTG
HC2-80	-----TCCAGCTTGACTACTCATTAAACAGATGAGTTCTGCAGAAACCACTTCTTGGTG
HC2B	CAAGACCTCCAGCTTGACTACTCATTAAACAGATGAGTTCTGCAGAAACCACTTCTTGGTG
HC2C	-----
HC2D-KIAA1058	CAAGACCTCCAGCTTGACTACTCATTAAACAGATGAGTTCTGCAGAAACCACTTCTTGGTG
HC2E	CAAGACCTCCAGCTTGACTACTCATTAAACAGATGAGTTCTGCAGAAACCACTTCTTGGTG
HC2F	-----

FIG. 3A (cont.)

HC2A	GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCCGGGAGGTCCGTCTGATC
HC2-80	GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCCGGGAGGTCCGTCTGATC
HC2B	GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCCGGGAGGTCCGTCTGATC
HC2C	-----
HC2D-KIAA1058	GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCCGGGAGGTCCGTCTGATC
HC2E	GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCCGGGAGGTCCGTCTGATC
HC2F	-----
HC2A	GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTTGATGACAGATATGCTTCA
HC2-80	GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTTGATGACAGATATGCTTCA
HC2B	GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTTGATGACAGATATGCTTCA
HC2C	-----
HC2D-KIAA1058	GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTTGATGACAGATATGCTTCA
HC2E	GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTTGATGACAGATATGCTTCA
HC2F	-----
HC2A	AGGAGCCATCAGGCAAGGATAGCCACCCTCTACCTGCCTCTGTTTGGTCTGCTGATTGAA
HC2-80	AGGAGCCATCAGGCAAGGATAGCCACCCTCTACCTGCCTCTGTTTGGTCTGCTGATTGAA
HC2B	AGGAGCCATCAGGCAAGGATAGCCACCCTCTACCTGCCTCTGTTTGGTCTGCTGATTGAA
HC2C	-----
HC2D-KIAA1058	AGGAGCCATCAGGCAAGGATAGCCACCCTCTACCTGCCTCTGTTTGGTCTGCTGATTGAA
HC2E	AGGAGCCATCAGGCAAGGATAGCCACCCTCTACCTGCCTCTGTTTGGTCTGCTGATTGAA
HC2F	-----
HC2A	AACGTCCAGCGGATCAATGTGAGGGATGTGTACCCCTTCCCTGTGAACGCGGGCATGACC
HC2-80	AACGTCCAGCGGATCAATGTGAGGGATGTGTACCCCTTCCCTGTGAACGCGGGCATGACC
HC2B	AACGTCCAGCGGATCAATGTGAGGGATGTGTACCCCTTCCCTGTGAACGCGGGCATGACC
HC2C	-----
HC2D-KIAA1058	AACGTCCAGCGGATCAATGTGAGGGATGTGTACCCCTTCCCTGTGAACGCGGGCATGACT
HC2E	AACGTCCAGCGGATCAATGTGAGGGATGTGTACCCCTTCCCTGTGAACGCGGGCATGACC
HC2F	-----
HC2A	GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGCAGAAGGGA
HC2-80	GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGCAGAAGGGA
HC2B	GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGCAGAAGGGA
HC2C	-----
HC2D-KIAA1058	GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGCAGAAGGGA
HC2E	GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGCAGAAGGGA
HC2F	-----
HC2A	AGCACCCCTGGACAACAGCCTGCACAAGGACCTGCTGGGCGCCATCTCCGGCATTGCTTCT
HC2-80	AGCACCCCTGGACAACAGCCTGCACAAGGACCTGCTGGGCGCCATCTCCGGCATTGCTTCT
HC2B	AGCACCCCTGGACAACAGCCTGCACAAGGACCTGCTGGGCGCCATCTCCGGCATTGCTTCT
HC2C	-----
HC2D-KIAA1058	AGCACCCCTGGACAACAGCCTGCACAAGGACCTGCTGGGCGCCATCTCCGGCATTGCTTCT
HC2E	AGCACCCCTGGACAACAGCCTGCACAAGGACCTGCTGGGCGCCATCTCCGGCATTGCTTCT
HC2F	-----

FIG. 3A (cont.)

HC2A	CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTTCGAGAGGATCT
HC2-80	CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTTCGAGAGGATCT
HC2B	CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTTCGAGAGGATCT
HC2C	-----
HC2D-KIAA1058	CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTTCGAGAGGATCT
HC2E	CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTTCGAGAGGATCT
HC2F	-----GCTGATTTCGAGAGGATCT
HC2A	CTCATAAGCACAGATTTCGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC
HC2-80	CTCATAAGCACAGATTTCGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC
HC2B	CTCATAAGCACAGATTTCGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC
HC2C	-----
HC2D-KIAA1058	CTCATAAGCACAGATTTCGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC
HC2E	CTCATAAGCACAGATTTCGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC
HC2F	CTCATAAGCACAGATTTCGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC
HC2A	CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCCGTGGTTCGCTGTGATAAACTT
HC2-80	CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCCGTGGTTCGCTGTGATAAACTT
HC2B	CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCCGTGGTTCGCTGTGATAAACTT
HC2C	-----
HC2D-KIAA1058	CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCCGTGGTTCGCTGTGATAAACTT
HC2E	CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCCGTGGTTCGCTGTGATAAACTT
HC2F	CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCCGTGGTTCGCTGTGATAAACTT
HC2A	GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTTCCCTCTACATCTTAAAGAGCATGTCT
HC2-80	GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTTCCCTCTACATCTTAAAGAGCATGTCT
HC2B	GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTTCCCTCTACATCTTAAAGAGCATGTCT
HC2C	-----
HC2D-KIAA1058	GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTTCCCTCTACATCTTAAAGAGCATGTCT
HC2E	GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTTCCCTCTACATCTTAAAGAGCATGTCT
HC2F	GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTTCCCTCTACATCTTAAAGAGCATGTCT
HC2A	GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACCTTATGGATTTTTTT
HC2-80	GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACCTTATGGATTTTTTT
HC2B	GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACCTTATGGATTTTTTT
HC2C	-----
HC2D-KIAA1058	GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACCTTATGGATTTTTTT
HC2E	GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACCTTATGGATTTTTTT
HC2F	GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACCTTATGGATTTTTTT
HC2A	ACAATATCTGAAGTCTGCCTGCACCAGTTCCAGTACATGGGGAAGCGATACATAGCCAGG
HC2-80	ACAATATCTGAAGTCTGCCTGCACCAGTTCCAGTACATGGGGAAGCGATACATAGCCAGG
HC2B	ACAATATCTGAAGTCTGCCTGCACCAGTTCCAGTACATGGGGAAGCGATACATAGCCAGG
HC2C	-----
HC2D-KIAA1058	ACAATATCTGAAGTCTGCCTGCACCAGTTCCAGTACATGGGGAAGCGATACATAGCCAGG
HC2E	ACAATATCTGAAGTCTGCCTGCACCAGTTCCAGTACATGGGGAAGCGATACATAGCCAGG
HC2F	ACAATATCTGAAGTCTGCCTGCACCAGTTCCAGTACATGGGGAAGCGATACATAGCCAGG

FIG. 3A (cont.)

HC2A	AACCAGGAGGGGTTGGGACCCATAGTTCATGATCGAAAGTCTCAGACATTGCCTGTTTCC
HC2-80	AACCAGGAGGGGTTGGGACCCATAGTTCATGATCGAAAGTCTCAGACATTGCCTGTTTCC
HC2B	AACCAGGAGGGGTTGGGACCCATAGTTCATGATCGAAAGTCTCAGACATTGCCTGTTTCC
HC2C	-----AA-----
HC2D-KIAA1058	AACCAGGAGGGGTTGGGACCCATAGTTCATGATCGAAAGTCTCAGACATTGCCTGTTTCC
HC2E	-----TGTGA-----GAAAG-----ATATCAAGTGT----
HC2F	
HC2A	CGTAACAGAACAGGAATGATGCATGCCAGATTGCAGCAGCTGGGCAGCCTGGATAACTCT
HC2-80	CGTAACAGAACAGGAATGATGCATGCCAGATTGCAGCAGCTGGGCAGCCTGGATAACTCT
HC2B	CGTAACAGAACAGGAATGATGCATGCCAGATTGCAGCAGCTGGGCAGCCTGGATAACTCT
HC2C	-----CAGGAATGATGCATGCCAGATTGCAGCAGCTGGGCAGCCTGGATAACTCT
HC2D-KIAA1058	CGTAACAGAACAGGAATGATGCATGCCAGATTGCAGCAGCTGGGCAGCCTGGATAACTCT
HC2E	-----GCTTGGA-----
HC2F	
HC2A	CTCACTTTTAACCACAGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT
HC2-80	CTCACTTTTAACCACAGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT
HC2B	CTCACTTTTAACCACAGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT
HC2C	-----
HC2D-KIAA1058	CTCACTTTTAACCACAGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT
HC2E	CTCACTTTTAACCACAGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT
HC2F	-TTTCTGTAGACAATGGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT
HC2A	GAAGCCAACATTGCTACTGAGGTTTGCCTGACAGCTCTGGACACGCTTTTCTCTATTTACA
HC2-80	GAAGCCAACATTGCTACTGAGGTTTGCCTGACAGCTCTGGACACGCTTTTCTCTATTTACA
HC2B	GAAGCCAACATTGCTACTGAGGTTTGCCTGACAGCTCTGGACACGCTTTTCTCTATTTACA
HC2C	-----
HC2D-KIAA1058	GAAGCCAACATTGCTACTGAGGTTTGCCTGACAGCTCTGGACACGCTTTTCTCTATTTACA
HC2E	GAAGCCAACATTGCTACTGAGGTTTGCCTGACAGCTCTGGACACGCTTTTCTCTATTTACA
HC2F	GAAGCCAACATTGCTACTGAGGTTTGCCTGACAGCTCTGGACACGCTTTTCTCTATTTACA
HC2A	TTGGCGTTTAAGAACCAGCTCCTGGCCGACCATGGACATAATCCTCTCATGAAAAAAGTT
HC2-80	TTGGCGTTTAAGAACCAGCTCCTGGCCGACCATGGACATAATCCTCTCATGAAAAAAGTT
HC2B	TTGGCGTTTAAG-----CTCCTGGCCGACCATGGACATAATCCTCTCATGAAAAAAGTT
HC2C	-----
HC2D-KIAA1058	TTGGCGTTTAAGAACCAGCTCCTGGCCGACCATGGACATAATCCTCTCATGAAAAAAGTT
HC2E	TTGGCGTTTAAGAACCAGCTCCTGGCCGACCATGGACATAATCCTCTCATGAAAAAAGTT
HC2F	TTGGCGTTTAAGAACCAGCTCCTGGCCGACCATGGACATAATCCTCTCATGAAAAAAGTT
HC2A	TTTGATGTCTACCTGTGTTTTCTTCAAAAACATCAGTCTGAAACGGCTTTAAAAAATGTC
HC2-80	TTTGATGTCTACCTGTGTTTTCTTCAAAAACATCAGTCTGAAACGGCTTTAAAAAATGTC
HC2B	TTTGATGTCTACCTGTGTTTTCTTCAAAAACATCAGTCTGAAACGGCTTTAAAAAATGTC
HC2C	-----
HC2D-KIAA1058	TTTGATGTCTACCTGTGTTTTCTTCAAAAACATCAGTCTGAAACGGCTTTAAAAAATGTC
HC2E	TTTGATGTCTACCTGTGTTTTCTTCAAAAACATCAGTCTGAAACGGCTTTAAAAAATGTC
HC2F	A-----

FIG. 3A (cont.)

HC2A	TTCAC TGCCTTAAGGTCCTTAATTTATAAGTTTCCCTCAACATTCTATGAAGGGAGAGCG
HC2-80	TTCAC TGCCTTAAGGTCCTTAATTTATAAGTTTCCCTCAACATTCTATGAAGGGAGAGCG
HC2B	TTCAC TGCCTTAAGGTCCTTAATTTATAAGTTTCCCTCAACATTCTATGAAGGGAGAGCG
HC2C	-----
HC2D-KIAA1058	TTCAC TGCCTTAAGGTCCTTAATTTATAAGTTTCCCTCAACATTCTATGAAGGGAGAGCG
HC2E	TTCAC TGCCTTAAGGTCCTTAATTTATAAGTTTCCCTCAACATTCTATGAAGGGAGAGCG
HC2F	-----
HC2A	GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTAAGTCCAAGCTGAGCTCC
HC2-80	GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTAAGTCCAAGCTGAGCTCC
HC2B	GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTAAGTCCAAGCTGAGCTCC
HC2C	-----
HC2D-KIAA1058	GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTAAGTCCAAGCTGAGCTCC
HC2E	GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTAAGTCCAAGCTGAGCTCC
HC2F	-----
HC2A	ATCAGGACGGAGGCCTCCAGCTGCTCTACTTCCTGATGAGGAACAACCTTTGATTACACT
HC2-80	ATCAGGACGGAGGCCTCCAGCTGCTCTACTTCCTGATGAGGAACAACCTTTGATTACACT
HC2B	ATCAGGACGGAGGCCTCCAGCTGCTCTACTTCCTGATGAGGAACAACCTTTGATTACACT
HC2C	-----
HC2D-KIAA1058	ATCAGGACGGAGGCCTCCAGCTGCTCTACTTCCTGATGAGGAACAACCTTTGATTACACT
HC2E	ATCAGGACGGAGGCCTCCAGCTGCTCTACTTCCTGATGAGGAACAACCTTTGATTACACT
HC2F	-----
HC2A	GGAAAGAAGTCCTTTGTCCGGACACATTTGCAAGTCATCATATCTGTGTCAGCCAGCTGATA
HC2-80	GGAAAGAAGTCCTTTGTCCGGACACATTTGCAAGTCATCATATCTGTGTCAGCCAGCTGATA
HC2B	GGAAAGAAGTCCTTTGTCCGGACACATTTGCAAGTCATCATATCTGTGTCAGCCAGCTGATA
HC2C	-----
HC2D-KIAA1058	GGAAAGAAGTCCTTTGTCCGGACACATTTGCAAGTCATCATATCTGTGTCAGCCAGCTGATA
HC2E	GGAAAGAAGTCCTTTGTCCGGACACATTTGCAAGTCATCATATCTGTGTCAGCCAGCTGATA
HC2F	-----
HC2A	GCAGACGTTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAC
HC2-80	GCAGACGTTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAC
HC2B	GCAGACGTTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAC
HC2C	-----
HC2D-KIAA1058	GCAGACGTTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAC
HC2E	GCAGACGTTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAC
HC2F	-----
HC2A	TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA
HC2-80	TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA
HC2B	TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA
HC2C	-----
HC2D-KIAA1058	TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA
HC2E	TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA
HC2F	-----

FIG. 3A (cont.)

HC2A	ACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCCAGATGAAGGAGCATGAGAACGAC
HC2-80	ACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCCAGATGAAGGAGCATGAGAACGAC
HC2B	ACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCCAGATGAAGGAGCATGAGAACGAC
HC2C	-----
HC2D-KIAA1058	ACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCCAGATGAAGGAGCATGAGAACGAC
HC2E	ACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCCAGATGAAGGAGCATGAGAACGAC
HC2F	-----
HC2A	CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCACGCCCCGAG
HC2-80	CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCACGCCCCGAG
HC2B	CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCACGCCCCGAG
HC2C	-----
HC2D-KIAA1058	CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCACGCCCCGAG
HC2E	CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCACGCCCCGAG
HC2F	-----
HC2A	CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA
HC2-80	CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA
HC2B	CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA
HC2C	-----
HC2D-KIAA1058	CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA
HC2E	CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA
HC2F	-----
HC2A	GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCACACGGAAA
HC2-80	GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCACACGGAAA
HC2B	GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCACACGGAAA
HC2C	-----
HC2D-KIAA1058	GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCACACGGAAA
HC2E	GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCACACGGAAA
HC2F	-----
HC2A	G-----
HC2-80	G-----
HC2B	G-----
HC2C	-----
HC2D-KIAA1058	GAAGCAGTCCAGTGGGAGCCGCCCTTCTCCCCACAGCCATAGCGCCTGCCTGAGGAGG
HC2E	G-----
HC2F	-----
HC2A	-----GCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAACATC
HC2-80	-----GCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAACATC
HC2B	-----GCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAACATC
HC2C	-----GTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAACATC
HC2D-KIAA1058	AGCCGGGGAGGCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAACATC
HC2E	-----GCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAACATC
HC2F	-----

FIG. 3A (cont.)

HC2A
 HC2-80
 HC2B
 HC2C
 HC2D-KIAA1058
 HC2E
 HC2F

GACGAGGAGGCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCAACGAGGAT
 GACGAGGAGGCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCAACGAGGAT
 GACGAGGAGGCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCAACGAGGAT
 GACGAGGAGGCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCAACGAGGAT
 GACGAGGAGGCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCAACGAGGAT
 GACGAGGAGGCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCAACGAGGAT
 GACGAGGAGGCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCAACGAGGAT

HC2A
 HC2-80
 HC2B
 HC2C
 HC2D-KIAA1058
 HC2E
 HC2F

GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAGCCGAGCGCTACGAG
 GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAGCCGAGCGCTACGAG
 GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAGCCGAGCGCTACGAG
 GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAGCCGAGCGCTACGAG
 GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAGCCGAGCGCTACGAG
 GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAGCCGAGCGCTACGAG
 GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAGCCGAGCGCTACGAG

HC2A
 HC2-80
 HC2B
 HC2C
 HC2D-KIAA1058
 HC2E
 HC2F

CTCATCGCCGACATCTACAACTTATCATCCCCATTTATGAGAAGCCGAGGGATTT----
 CTCATCGCCGACATCTACAACTTATCATCCCCATTTATGAGAAGCCGAGGGATTT----
 CTCATCGCCGACATCTACAACTTATCATCCCCATTTATGAGAAGCCGAGGGATTTTGAG
 CTCATCGCCGACATCTACAACTTATCATCCCCATTTATGAGAAGCCGAGGGATTTTGAG
 CTCATTGCCGACATCTACAACTTATCATCCCCATTTATGAGAAGCCGAGGGATTTTGAG
 CTCATCGCCGACATCTACAACTTATCATCCCCATTTATGAGAAGCCGAGGGATTTTGAG
 CTCATCGCCGACATCTACAACTTATCATCCCCATTTATGAGAAGCCGAGGGATTTTGAG

HC2A
 HC2-80
 HC2B
 HC2C
 HC2D-KIAA1058
 HC2E
 HC2F

AGGCTGGCCCATCTGTATGACACGCTGCACCGGGCCTACAGCAAAGTGACCGAGGTCATG
 AGGCTGGCCCATCTGTATGACACGCTGCACCGGGCCTACAGCAAAGTGACCGAGGTCATG
 AGGCTGGCCCATCTGTATGACACGCTGCACCGGGCCTACAGCAAAGTGACCGAGGTCATG
 AGGCTGGCCCATCTGTATGACACGCTGCACCGGGCCTACAGCAAAGTGACCGAGGTCATG
 AGGCTGGCCCATCTGTATGACACGCTGCACCGGGCCTACAGCAAAGTGACCGAGGTCATG
 AGGCTGGCCCATCTGTATGACACGCTGCACCGGGCCTACAGCAAAGTGACCGAGGTCATG
 AGGCTGGCCCATCTGTATGACACGCTGCACCGGGCCTACAGCAAAGTGACCGAGGTCATG

HC2A
 HC2-80
 HC2B
 HC2C
 HC2D-KIAA1058
 HC2E
 HC2F

CACTCGGGCCGAGGCTTCTGGGGACCTACTTCCGGGTAGCCTTCTTCGGGCAGG----
 CACTCGGGCCGAGGCTTCTGGGGACCTACTTCCGGGTAGCCTTCTTCGGGCAGG----
 CACTCGGGCCGAGGCTTCTGGGGACCTACTTCCGGGTAGCCTTCTTCGGGCAGG----
 CACTCGGGCCGAGGCTTCTGGGGACCTACTTCCGGGTAGCCTTCTTCGGGCAGG----
 CACTCGGGCCGAGGCTTCTGGGGACCTACTTCCGGGTAGCCTTCTTCGGGCAGG----
 CACTCGGGCCGAGGCTTCTGGGGACCTACTTCCGGGTAGCCTTCTTCGGGCAGG----
 CACTCGGGCCGAGGCTTCTGGGGACCTACTTCCGGGTAGCCTTCTTCGGGCAGG----

HC2A
 HC2-80
 HC2B
 HC2C
 HC2D-KIAA1058
 HC2E
 HC2F

CTTTGAAGATGAAGATGGA
 CTTTGAAGATGAAGATGGA
 GATTCTTTGAAGATGAAGATGGA
 GATTCTTTGAAGATGAAGATGGA
 CAATACCAGTTTACAGACAGTGAAACAGATGTGGAGGGATCTTTGAAGATGAAGATGGA
 GATTCTTTGAAGATGAAGATGGA
 GATTCTTTGAAGATGAAGATGGA

FIG. 3A (cont.)

HC2A	AAGGAGTATATTTACAAGGAACCCAAACTCACACCGCTGTCTCGGAAATTTCTCAGAGACTC
HC2-80	AAGGAGTATATTTACAAGGAACCCAAACTCACACCGCTGTCTCGGAAATTTCTCAGAGACTC
HC2B	AAGGAGTATATTTACAAGGAACCCAAACTCACACCGCTGTCTCGGAAATTTCTCAGAGACTC
HC2C	AAGGAGTATATTTACAAGGAACCCAAACTCACACCGCTGTCTCGGAAATTTCTCAGAGACTC
HC2D-KIAA1058	AAGGAGTATATTTACAAGGAACCCAAACTCACACCGCTGTCTCGGAAATTTCTCAGAGACTC
HC2E	AAGGAGTATATTTACAAGGAACCCAAACTCACACCGCTGTCTCGGAAATTTCTCAGAGACTC
HC2F	-----
HC2A	CTTAAACTGTACTCGGATAAAATTTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC
HC2-80	CTTAAACTGTACTCGGATAAAATTTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC
HC2B	CTTAAACTGTACTCGGATAAAATTTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC
HC2C	CTTAAACTGTACTCGGATAAAATTTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC
HC2D-KIAA1058	CTTAAACTGTACTCGGATAAAATTTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC
HC2E	CTTAAACTGTACTCGGATAAAATTTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC
HC2F	-----
HC2A	AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC
HC2-80	AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC
HC2B	AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC
HC2C	AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC
HC2D-KIAA1058	AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCCTACATCCAGGTGACTCACGTCATC
HC2E	AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC
HC2F	-----
HC2A	CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAACAGAGTTTGAGAGATCCCAACAAC
HC2-80	CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAACAGAGTTTGAGAGATCCCAACAAC
HC2B	CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAACAGAGTTTGAGAGATCCCAACAAC
HC2C	CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAACAGAGTTTGAGAGATCCCAACAAC
HC2D-KIAA1058	CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAACAGAGTTTGAGAGATCCCAACAAC
HC2E	CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAACAGAGTTTGAGAGATCCCAACAAC
HC2F	-----
HC2A	ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG
HC2-80	ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG
HC2B	ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG
HC2C	ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG
HC2D-KIAA1058	ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG
HC2E	ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG
HC2F	-----
HC2A	GAAGAGCAGTGCAAACGGCGCACCATCCTGACAGCCATACACTGCTTCCCTTATGTGAAG
HC2-80	GAAGAGCAGTGCAAACGGCGCACCATCCTGACAGCCATACACTGCTTCCCTTATGTGAAG
HC2B	GAAGAGCAGTGCAAACGGCGCACCATCCTGACAGCCATACACTGCTTCCCTTATGTGAAG
HC2C	GAAGAGCAGTGCAAACGGCGCACCATCCTGACAGCCATACACTGCTTCCCTTATGTGAAG
HC2D-KIAA1058	GAAGAGCAGTGCAAACGGCGCACCATCCTGACAGCCATACACTGCTTCCCTTATGTGAAG
HC2E	GAAGAGCAGTGCAAACGGCGCACCATCCTGACAGCCATACACTGCTTCCCTTATGTGAAG
HC2F	-----

FIG. 3A (cont.)

HC2A	AAGCGCATCCCTGTTCATGTACCAGCACCACACTGACCTGAACCCCCATCGAGGTGGCCATT
HC2-80	AAGCGCATCCCTGTTCATGTACCAGCACCACACTGACCTGAACCCCCATCGAGGTGGCCATT
HC2B	AAGCGCATCCCTGTTCATGTACCAGCACCACACTGACCTGAACCCCCATCGAGGTGGCCATT
HC2C	AAGCGCATCCCTTTTCATGTACCAGCACCACACTGACCTGAACCCCCATCGAGGT--CCATT
HC2D-KIAA1058	AAGCGCATCCCTGTTCATGTACCAGCACCACACTGACCTGAACCCCCATCGAGGTGGCCATT
HC2E	AAGCGCATCCCTGTTCATGTACCAGCACCACACTGACCTGAACCCCCATCGAGGTGGCCATT
HC2F	-----
HC2A	GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC
HC2-80	GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC
HC2B	GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC
HC2C	GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC
HC2D-KIAA1058	GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC
HC2E	GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC
HC2F	-----
HC2A	ATGATCAAACCTGCAGCTCAAACCTCCAGGGCAGCGTGAGTGTTCAAGTCAATGCTGGCCCCA
HC2-80	ATGATCAAACCTGCAGCTCAAACCTCCAGGGCAGCGTGAGTGTTCAAGTCAATGCTGGCCCCA
HC2B	ATGATCAAACCTGCAGCTCAAACCTCCAGGGCAGCGTGAGTGTTCAAGTCAATGCTGGCCCCA
HC2C	ATGATCAAACCTGCAGCTCAAACCTCCAGGGCAGCGTGAGTGTTCAAGTCAATGCTGGCCCCA
HC2D-KIAA1058	ATGATCAAACCTGCAGCTCAAACCTCCAGGGCAGCGTGAGTGTTCAAGTCAATGCTGGCCCCA
HC2E	ATGATCAAACCTGCAGCTCAAACCTCCAGGGCAGCGTGAGTGTTCAAGTCAATGCTGGCCCCA
HC2F	-----
HC2A	CTAGCATATGCGCGAGCTTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA
HC2-80	CTAGCATATGCGCGAGCTTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA
HC2B	CTAGCATATGCGCGAGCTTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA
HC2C	CTAGCATATGCGCGAGCTTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA
HC2D-KIAA1058	CTAGCATATGCGCGAGCTTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA
HC2E	CTAGCATATGCGCGAGCTTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA
HC2F	-----
HC2A	GTGAAGCTGCTTAAGGAAGTTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG
HC2-80	GTGAAGCTGCTTAAGGAAGTTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG
HC2B	GTGAAGCTGCTTAAGGAAGTTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG
HC2C	GTGAAGCTGCTTAAGGAAGTTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG
HC2D-KIAA1058	GTGAAGCTGCTTAAGGAAGTTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG
HC2E	GTGAAGCTGCTTAAGGAAGTTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG
HC2F	-----
HC2A	GTAAACGAACGTCTGATTAAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAAC
HC2-80	GTAAACGAACGTCTGATTAAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAAC
HC2B	GTAAACGAACGTCTGATTAAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAAC
HC2C	GTAAACGAACGTCTGATTAAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAAC
HC2D-KIAA1058	GTAAACGAACGTCTGATTAAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAAC
HC2E	GTAAACGAACGTCTGATTAAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAAC
HC2F	-----

FIG. 3A (cont.)

HC2A	TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAG-----ATCTGCC
HC2-80	TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAG-----ATCTGCC
HC2B	TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAG-----ATCTGCC
HC2C	TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAG-----ATCTGCC
HC2D-KIAA1058	TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAGCTGGGATGATCTGCC
HC2E	TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAG-----ATCTGCC
HC2F	-----
HC2A	CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACATCTTCAACGCCATCAGTG
HC2-80	CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACATCTTCAACGCCATCAGTG
HC2B	CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACATCTTCAACGCCATCAGTG
HC2C	CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACATCTTCAACGCCATCAGTG
HC2D-KIAA1058	CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACATCTTCAACGCCATCAGTG
HC2E	CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACATCTTCAACGCCATCAGTG
HC2F	-----
HC2A	GGACTCCAACAAGCACAATGGTTACGGGATGACCAGCTCGTCTTCGGTCGTGTGATTAC
HC2-80	GGACTCCAACAAGCACAATGGTTACGGGATGACCAGCTCGTCTTCGGTCGTGTGATTAC
HC2B	GGACTCCAACAAGCACAATGGTTACGGGATGACCAGCTCGTCTTCGGTCGTGTGA----
HC2C	GGACTCCAACAAGCACAATGGTTACGGGATGACCAGCTCGTCTTCGGTCGTGTGA----
HC2D-KIAA1058	GGACTCCAACAAGCACAATGGTTACGGGATGACCAGCTCGTCTTCGGTCGTGTGATTAC
HC2E	GGACTCCAACAAGCACAATGGTTACGGGATGACCAGCTCGTCTTCGGTCGTGTGA----
HC2F	-----
HC2A	ATCTCATGGCCCCGTGTGTGGGGACTTGCTTTGTGCAATTTGCAAACCTCAGGATGCTTTCCAA
HC2-80	ATCTCATGGCCCCGTGTGTGGGGACTTGCTTTGTGCAATTTGCAAACCTCAGGATGCTTTCCAA
HC2B	-----
HC2C	-----
HC2D-KIAA1058	ATCTCATGGCCCCGTGTGTGGGGACTTGCTTTGTGCAATTTGCAAACCTCAGGATGCTTTCCAA
HC2E	-----
HC2F	-----
HC2A	AGCCAATCACTGGGGAGACCGAGCACAGGGAGGACCAAGGGGAAGGGGAGAGAAAGGAAA
HC2-80	AGCCAATCACTGGGGAGACCGAGCACAGGGAGGACCAAGGGGAAGGGGAGAGAAAGGAAA
HC2B	-----
HC2C	-----
HC2D-KIAA1058	AGCCAATCACTGGGGAGACCGAGCACAGGGAGGACCA--GGGGAAGGGGAGAGAAAGGAAA
HC2E	-----
HC2F	-----
HC2A	TAAAGAACAACGTTATTTCTTAACAGACTTTCTATAGGAGTTGTAAGAAGGTGCACATAT
HC2-80	TAAAGAACAACGTTATTTCTTAACAGACTTTCTATAGGAGTTGTAAGAAGGTGCACATAT
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TAAAGAACAACGTTATTTCTTAACAGACTTTCTATAGGAGTTGTAAGAAGGTGCACATAT
HC2E	-----
HC2F	-----

FIG. 3A (cont.)

HC2A	TTTTTTAAATCTCACTGGCAATATTCAAAGTTTTTCATTGTGTCTTAACAAAGGTGTGGTA
HC2-80	TTTTTTAAATCTCACTGGCAATATTCAAAGTTTTTCATTGTGTCTTAACAAAGGTGTGGTA
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TTTTTTAAATCTCACTGGCAATATTCAAAGTTTTTCATTGTGTCTTAACAAAGGTGTGGTA
HC2E	-----
HC2F	-----
HC2A	GACACTCTTGAGCTGGACTTAGATTTTATTCTTCCTTGCAGAGTAGTGTTAGAATAGATG
HC2-80	GACACTCTTGAGCTGGACTTAGATTTTATTCTTCCTTGCAGAGTAGTGTTAGAATAGATG
HC2B	-----
HC2C	-----
HC2D-KIAA1058	GACACTCTTGAGCTGGACTTAGATTTTATTCTTCCTTGCAGAGTAGTGTTAGAATAGATG
HC2E	-----
HC2F	-----
HC2A	GCCTACAGAAAAAAGGTTCTGGGATCTACATGGCAGGGAGGGCTGCACTGACATTGAT
HC2-80	GCCTACAGAAAAAAGGTTCTGGGATCTACATGGCAGGGAGGGCTGCACTGACATTGAT
HC2B	-----
HC2C	-----
HC2D-KIAA1058	GCCTACAGAAAAAAGGTTCTGGGATCTACATGGCAGGGAGGGCTGCACTGACATTGAT
HC2E	-----
HC2F	-----
HC2A	GCCTGGGGGACCTTTTGCCTCGACTCGTGCCGAAATCTGATCGTAATCAGGGTACAGAA
HC2-80	GCCTGGGGGACCTTTTGCCTCGACTCGTGCCGAAATCTGATCGTAATCAGGGTACAGAA
HC2B	-----
HC2C	-----
HC2D-KIAA1058	GCCTGGGGGACCTTTTGCCTCGAGGCTGAGCTGGAAAATCTTGAAAATATTTTTTT---T
HC2E	-----
HC2F	-----
HC2A	CTTACTAGTTTTGTCTAGGAGTATGTTGTATGACTAGGATTTGTGCTATTATCTCATTCA
HC2-80	CTTACTAGTTTTGTCTAGGAGTATGTTGTATGACTAGGATTTGTGCTATTATCTCATTCA
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TTTCCTGTGGCACATTCAGGTTGAATACAAGAACTATTTTTGTGACTAGTTTTTGTATGAC
HC2E	-----
HC2F	-----
HC2A	ACAACATAGAGCAAGAATAGTGAGCTAACTGAGCTAGACACTCAATTAATCCGCTACTGG
HC2-80	ACAACATAGAGCAAGAATAGTGAGCTAACTGAGCTAGACACTCAATTAATCCGCTACTGG
HC2B	-----
HC2C	-----
HC2D-KIAA1058	CTAAGGGAAGTGAACATTGTAATTTTTGTACCAGTGAACCAGGAGATTTAGTGCTTTTAT
HC2E	-----
HC2F	-----

FIG. 3A (cont.)

HC2A	CTTCAAGTCAGAACTTTGTCATTAATCATCGACTCCGGGACGGTCATATATGTATTACAT
HC2-80	CTTCAAGTCAGAACTTTGTCATTAATCATCGACTCCGGGACGGTCATATATGTATTACAT
HC2B	-----
HC2C	-----
HC2D-KIAA1058	ATTCATTTTCCTTGCAATTAAGAAAATATGAAAGCTTAAGGAATTATGTGAGCTTAAACT
HC2E	-----
HC2F	-----
HC2A	TTCTACATTTTTAATACTCACATGGGCTTATGCATTAAGTTTAATTGTGATAAATTTGTG
HC2-80	TTCTACATTTTTAATACTCACATGGGCTTATGCATTAAGTTTAATTGTGATAAATTTGTG
HC2B	-----
HC2C	-----
HC2D-KIAA1058	AGTCAAGCAGTTTAGAACCAAAGGCCTATATTAATAACCGCAACTATGCTGAAAAGTACA
HC2E	-----
HC2F	-----
HC2A	CTGGTCCAGTATATGCAATACACTTTAATGGTTTATTCTTGTCATAAAAATGTGCAATAT
HC2-80	CTGGTCCAGTATATGCAATACACTTTAATGGTTTATTCTTGTCATAAAAATGTGCAATAT
HC2B	-----
HC2C	-----
HC2D-KIAA1058	AAGTAGTACAGTATATTGTTATGTACATATCATTGTTAATACAGTCCTGGCATTCTGTAC
HC2E	-----
HC2F	-----
HC2A	GGAGATGTATACAAGTCTTTACT-----
HC2-80	GGAGATGTATACAAGTCTTTACT-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	ATATATGTATTACATTTCTACATTTTTAATACTCACATGGGCTTATGCATTAAGTTTAAT
HC2E	-----
HC2F	-----
HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TGTGATAAATTTGTGCTGTTCCAGTATATGCAATACACTTTAATGTTTTATTCTTGTACA
HC2E	-----
HC2F	-----
HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TAAAAATGTGCAATATGGAGATGTATACAGTCTTTACTATATTAGGTTTATAAACAGTTT
HC2E	-----
HC2F	-----

FIG. 3A (cont.)

HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TAAGAATTTTCATCCTTTTGCCAAAATGGTGGAGTATGTAATTGGTAAATCATAAATCCTG
HC2E	-----
HC2F	-----
HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TGGTGAATGGTGGTGTACTTTAAAGCTGTCACCATGTTATATTTTCTTTTAAGACATTAA
HC2E	-----
HC2F	-----
HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TTTAGTAATTTTATATTTGGGAAAATAAAGGTTTTTAATTTTATTTAACTGGAATCACTG
HC2E	-----
HC2F	-----
HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	CCCTGCTGTAATTAAACATTCTGTACCACATCTGTATTAAAAAGACATTGCTGACC
HC2E	-----
HC2F	-----

FIG. 3A (cont.)

HC2A	CTTCAAGTCAGAACTTTGTCATTAATCATCGACTCCGGGACGGTCATATATGTATTACAT
HC2-80	CTTCAAGTCAGAACTTTGTCATTAATCATCGACTCCGGGACGGTCATATATGTATTACAT
HC2B	-----
HC2C	-----
HC2D-KIAA1058	ATTCATTTCCCTTGCAATTTAAGAAAATATGAAAGCTTAAGGAATTATGTGAGCTTAAACT
HC2E	-----
HC2F	-----

HC2A	TTCTACATTTTAAATACTCACATGGGCTTATGCATTAAGTTTAAATTGTGATAAAATTTGTG
HC2-80	TTCTACATTTTAAATACTCACATGGGCTTATGCATTAAGTTTAAATTGTGATAAAATTTGTG
HC2B	-----
HC2C	-----
HC2D-KIAA1058	AGTCAAGCAGTTTAGAACCAAAGGCCTATATTAATAACCGCAACTATGCTGAAAAGTACA
HC2E	-----
HC2F	-----

HC2A	CTGGTCCAGTATATGCAATACACTTTAATGGTTTATTCTTGTCATAAAAATGTGCAATAT
HC2-80	CTGGTCCAGTATATGCAATACACTTTAATGGTTTATTCTTGTCATAAAAATGTGCAATAT
HC2B	-----
HC2C	-----
HC2D-KIAA1058	AAGTAGTACAGTATATTGTTATGTACATATCATTGTTAATACAGTCCTGGCATTCTGTAC
HC2E	-----
HC2F	-----

HC2A	GGAGATGTATACAAGTCTTTACT-----
HC2-80	GGAGATGTATACAAGTCTTTACT-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	ATATATGTATTACATTTCTACATTTTTAATACTCACATGGGCTTATGCATTAAGTTTAAAT
HC2E	-----
HC2F	-----

HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TGTGATAAATTTGTGCTGTTCCAGTATATGCAATACACTTTAATGTTTTATTCTTGTTACA
HC2E	-----
HC2F	-----

HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TAAAAATGTGCAATATGGAGATGTATACAGTCTTTACTATATTAGGTTTATAAACAGTTT
HC2E	-----
HC2F	-----

FIG. 3A (cont.)

HC2A
HC2-80
HC2B
HC2C
HC2D-KIAA1058 TAAGAATTTTCATCCTTTTGCCAAAATGGTGGAGTATGTAATTGGTAAATCATAAATCCTG
HC2E
HC2F

HC2A
HC2-80
HC2B
HC2C
HC2D-KIAA1058 TGGTGAATGGTGGTGTACTTTAAAGCTGTCACCATGTTATATTTTCTTTTAAGACATTAA
HC2E
HC2F

HC2A
HC2-80
HC2B
HC2C
HC2D-KIAA1058 TTTAGTAATTTTATATTTGGGAAAATAAAGGTTTTTAATTTTATTAACTGGAATCACTG
HC2E
HC2F

HC2A
HC2-80
HC2B
HC2C
HC2D-KIAA1058 CCCTGCTGTAATTAAACATTCTGTACCACATCTGTATTAAAAAGACATTGCTGACC
HC2E
HC2F

HC2A	-----
HC2A-80	-----
HC2B	-----
HC2C	-----
HC2D	ASGNLDKNARFSAIYRQDSNKLSDNDMLKLIADFRKPEKMAKLPVILGNLDITIDNVSSD
HC2E	-----
HC2F	-----
HC2A	-----
HC2A-80	-----
HC2B	-----
HC2C	-----
HC2D	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVPKYLKYDSQ
HC2E	-----
HC2F	-----
HC2A	-----VLHHHQNPFEFYDEIK
HC2A-80	-----
HC2B	-----
HC2C	-----
HC2D	KSAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTSAFAAVLHHHQNPFEFYDEIK
HC2E	-----
HC2F	-----
HC2A	IELPTQLHEKHLLLLTFFHVSCDNSSKSGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
HC2A-80	-----
HC2B	-----
HC2C	-----
HC2D	IELPTQLHEKHLLLLTFFHVSCDNSSKSGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
HC2E	-----
HC2F	-----
HC2A	PVSANLPSGYLGQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFQYC
HC2A-80	-----
HC2B	-----
HC2C	-----
HC2D	PVSANLPSGYLGQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFQYC
HC2E	-----
HC2F	-----
HC2A	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLTRATQEEVAVNVTRVI
HC2A-80	-----
HC2B	-----AMEGHVMIAFLPTILNQLFRVLTRATQEEVAVNVTRVI
HC2C	-----
HC2D	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLTRATQEEVAVNVTRVI
HC2E	-----AMEGHVMIAFLPTILNQLFRVLTRATQEEVAVNVTRVI
HC2F	-----

Fig. 3B

HC2A	IHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSNK
HC2A-80	-----
HC2B	IHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSNK
HC2C	-----
HC2D	IHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSNK
HC2E	IHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSNK
HC2F	-----
HC2A	LLRYSWFFFDVLIKSMQHLIENSKVKLLRNQRFPPASYHHAAETVVNMLMPHITQKFGDN
HC2A-80	-----
HC2B	LLRYSWFFFDVLIKSMQHLIENSKVKLLRNQRFPPASYHHAAETVVNMLMPHITQKFGDN
HC2C	-----
HC2D	LLKYSWFFFDVLIKSMQHLIENSKVKLLRNQRFPPASYHHAAETVVNMLMPHITQKFRDN
HC2E	LLRYSWFFFDVLIKSMQHLIENSKVKLLRNQRFPPASYHHAAETVVNMLMPHITQKFGDN
HC2F	-----
HC2A	PEASKNANHSLAVFIKRCFTFMDRGFVFKQINNYISCFAPGDPKTLFEYKFEFLRVVCNH
HC2A-80	-----
HC2B	PEASKNANHSLAVFIKRCFTFMDRGFVFKQINNYISCFAPGDPKTLFEYKFEFLRVVCNH
HC2C	-----
HC2D	PEASKNANHSLAVFIKRCFTFMDRGFVFKQINNYISCFAPGDPKTLFEYKFEFLRVVCNH
HC2E	PEASKNANHSLAVFIKRCFTFMDRGFVFKQINNYISCFAPGDPKTLFEYKFEFLRVVCNH
HC2F	-----
HC2A	EHYIPLNLPMPFGKGRIQRYQDLQLDYSLTDEFCRNHFLVGLLLREVG TALQEFREVRLI
HC2A-80	-----QLDYSLTDEFCRNHFLVGLLLREVG TALQEFREVRLI
HC2B	EHYIPLNLPMPFGKGRIQRYQDLQLDYSLTDEFCRNHFLVGLLLREVG TALQEFREVRLI
HC2C	-----
HC2D	EHYIPLNLPMPFGKGRIQRYQDLQLDYSLTDEFCRNHFLVGLLLREVG TALQEFREVRLI
HC2E	EHYIPLNLPMPFGKGRIQRYQDLQLDYSLTDEFCRNHFLVGLLLREVG TALQEFREVRLI
HC2F	-----
HC2A	AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPFPVNAGMT
HC2A-80	AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPFPVNAGMT
HC2B	AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPFPVNAGMT
HC2C	-----
HC2D	AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPFPVNAGMT
HC2E	AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPFPVNAGMT
HC2F	-----
HC2A	VKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTTSTPNINSVRNADSRGS
HC2A-80	VKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTTSTPNINSVRNADSRGS
HC2B	VKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTTSTPNINSVRNADSRGS
HC2C	-----
HC2D	VKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTTSTPNINSVRNADSRGS
HC2E	VKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTTSTPNINSVRNADSRGS
HC2F	-----ADSRGS

FIG. 3B (cont.)

HC2A	LISTDSGNSLPERNSEKSNSLDKHQSSSTLGNSVVRCDKLDQSEIKSLLMCFLYILKSMS
HC2A-80	LISTDSGNSLPERNSEKSNSLDKHQSSSTLGNSVVRCDKLDQSEIKSLLMCFLYILKSMS
HC2B	LISTDSGNSLPERNSEKSNSLDKHQSSSTLGNSVVRCDKLDQSEIKSLLMCFLYILKSMS
HC2C	-----
HC2D	LISTDSGNSLPERNSEKSNSLDKHQSSSTLGNSVVRCDKLDQSEIKSLLMCFLYILKSMS
HC2E	LISTDSGNSLPERNSEKSNSLDKHQSSSTLGNSVVRCDKLDQSEIKSLLMCFLYILKSMS
HC2F	LISTDSGNSLPERNSEKSNSLDKHQSSSTLGNSVVRCDKLDQSEIKSLLMCFLYILKSMS
HC2A	DDALFTYWNKASTSEIMDFFTISEVCLHQFQYMGKRYIARNQEGLGPIVHDKRSQTLFVS
HC2A-80	DDALFTYWNKASTSEIMDFFTISEVCLHQFQYMGKRYIARNQEGLGPIVHDKRSQTLFVS
HC2B	DDALFTYWNKASTSEIMDFFTISEVCLHQFQYMGKRYIARNQEGLGPIVHDKRSQTLFVS
HC2C	-----
HC2D	DDALFTYWNKASTSEIMDFFTISEVCLHQFQYMGKRYIAR-----
HC2E	DDALFTYWNKASTSEIMDFFTISEVCLHQFQYMGKRYIARNQEGLGPIVHDKRSQTLFVS
HC2F	DDALFTYWNKASTSEIMDFFTISEVCLHQFQYMGKRYIAS-----VR--KISSVLGIS
HC2A	RNRTGMMHARLQQLGSLDNSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT
HC2A-80	RNRTGMMHARLQQLGSLDNSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT
HC2B	RNRTGMMHARLQQLGSLDNSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT
HC2C	-----
HC2D	---TGMHARLQQLGSLDNSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT
HC2E	RNRTGMMHARLQQLGSLDNSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT
HC2F	V-----D-NG-----YGHSDADVLHQSLLEANIATEVCLTALDTLSLFT
HC2A	LAFKNQLLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFYEGRA
HC2A-80	LAFKNQLLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFYEGRA
HC2B	LAFK--LLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFYEGRA
HC2C	-----
HC2D	LAFKNQLLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFYEGRA
HC2E	LAFKNQLLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFYEGRA
HC2F	LAFKNQLLADHGHNPMLKKK-----
HC2A	DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTHLQVII SVSqli
HC2A-80	DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTHLQVII SVSqli
HC2B	DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTHLQVII SVSqli
HC2C	-----
HC2D	DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTHLQVII SVSqli
HC2E	DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTHLQVII SVSqli
HC2F	-----
HC2A	ADVVGIGETRFQQSLSIINNCANSRLIKHTSFSSDVKDLTRIRTVLMATAQMKEHEND
HC2A-80	ADVVGIGETRFQQSLSIINNCANSRLIKHTSFSSDVKDLTRIRTVLMATAQMKEHEND
HC2B	ADVVGIGETRFQQSLSIINNCANSRLIKHTSFSSDVKDLTRIRTVLMATAQMKEHEND
HC2C	-----
HC2D	ADVVGIGETRFQQSLSIINNCANSRLIKHTSFSSDVKDLTRIRTVLMATAQMKEHEND
HC2E	ADVVGIGETRFQQSLSIINNCANSRLIKHTSFSSDVKDLTRIRTVLMATAQMKEHEND
HC2F	-----

FIG. 3B (cont.)

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HC2A	PEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKN GDLSEAAMCYVHV TALVAEYLTRK
HC2A-80	PEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKN GDLSEAAMCYVHV TALVAEYLTRK
HC2B	PEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKN GDLSEAAMCYVHV TALVAEYLTRK
HC2C	-----
HC2D	PEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKN GDLSEAAMCYVHV TALVAEYLTRK
HC2E	PEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKN GDLSEAAMCYVHV TALVAEYLTRK
HC2F	-----
HC2A	-----GVFRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE
HC2A-80	-----GVFRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE
HC2B	-----GVFRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE
HC2C	-----FRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE
HC2D	EAVQWEPPLPHSHSACLRRSRGGVFRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE
HC2E	-----GVFRQGCTAFRVITPNIDEEASMMEDVG-----
HC2F	-----
HC2A	DVIMELLEQCADGLWKAERYELIADIYKLIIP IYEKRR-----
HC2A-80	DVIMELLEQCADGLWKAERYELIADIYKLIIP IYEKRR-----
HC2B	DVIMELLEQCADGLWKAERYELIADIYKLIIP IYEKRRD FERLAHLYDTLHRAYSK
HC2C	DVIMELLEQCADGLWKAERYELIADIYKLIIP IYEKRRD FERLAHLYDTLHRAYSK
HC2D	DVIMELLEQCADGLWKAERYELIADIYKLIIP IYEKRRD FERLAHLYDTLHRAYSK
HC2E	-----KAERYELIADIYKLIIP IYEKRRD FERLAHLYDTLHRAYSK
HC2F	-----
HC2A	-----DFFEDEDGKEYIYKEPKLTPLSE
HC2A-80	-----DFFEDEDGKEYIYKEPKLTPLSE
HC2B	VTEVMHSGRRLLGTYFRVAFFG-----QGFFEDEDGKEYIYKEPKLTPLSE
HC2C	VTEVMHSGRRLLGTYFRVAFFG-----QGFFEDEDGKEYIYKEPKLTPLSE
HC2D	VTEVMHSGRRLLGTYFRVAFFGQAAQYQFTDSETDVEGFFEDEDGKEYIYKEPKLTPLSE
HC2E	VTEVMHSGRRLLGTYFRVAFFG-----QGFFEDEDGKEYIYKEPKLTPLSE
HC2F	-----
HC2A	ISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLD SKYAYIQVTHVIPFFDEKELQERKTEF
HC2A-80	ISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLD SKYAYIQVTHVIPFFDEKELQERKTEF
HC2B	ISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLD SKYAYIQVTHVIPFFDEKELQERKTEF
HC2C	ISQRLLKLYSDKFGSENVKMTQDSGKVNPKDLD SKYAYIQVTHVIPFFDEKELQERKTEF
HC2D	ISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLD SKYAYIQVTHVIPFFDEKELQERKTEF
HC2E	ISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLD SKYAYIQVTHVIPFFDEKELQERKTEF
HC2F	-----
HC2A	ERSHNIRRFMFEMPFTQTGKRQGGVVEEQCKRR TILTAIHCFPYVKKRIPVMYQHHTDLNP
HC2A-80	ERSHNIRRFMFEMPFTQTGKRQGGVVEEQCKRR TILTAIHCFPYVKKRIPVMYQHHTDLNP
HC2B	ERSHNIRRFMFEMPFTQTGKRQGGVVEEQCKRR TILTAIHCFPYVKKRIPVMYQHHTDLNP
HC2C	ERSHNIRRFMFEMPFTQTGKRQGGVVEEQCKRR TILTAIHCFPYVKKRIPFMYQHHTDLNP
HC2D	ERSHNIRRFMFEMPFTQTGKRQGGVVEEQCKRR TILTAIHCFPYVKKRIPVMYQHHTDLNP
HC2E	ERSHNIRRFMFEMPFTQTGKRQGGVVEEQCKRR TILTAIHCFPYVKKRIPVMYQHHTDLNP
HC2F	-----

FIG. 3B (cont.)

HC2A	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSVSVQVNAGPLAYARAFLLDDTNTKR
HC2A-80	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSVSVQVNAGPLAYARAFLLDDTNTKR
HC2B	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSVSVQVNAGPLAYARAFLLDDTNTKR
HC2C	IEVHZ-----
HC2D	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSVSVQVNAGPLAYARAFLLDDTNTKR
HC2E	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSVSVQVNAGPLAYARAFLLDDTNTKR
HC2F	-----
HC2A	YPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQ
HC2A-80	YPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQ
HC2B	YPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQ
HC2C	-----
HC2D	YPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQ
HC2E	YPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQ
HC2F	-----
HC2A	ICPLEEKTSVLPNSLHIFNAISGTPPTSTMVHGMTSSSSSVVZ----
HC2A-80	ICPLEEKTSVLPNSLHIFNAISGTPPTSTMVHGMTSSSSSVVZ----
HC2B	ICPLEEKTSVLPNSLHIFNAISGTPPTSTMVHGMTSSSSSVVZ----
HC2C	-----
HC2D	LG-----
HC2E	ICPLEEKTSVLPNSLHIFNAISGTPPTSTMVHGMTSSSSSVVZ----
HC2F	-----

FIG. 3B (cont.)

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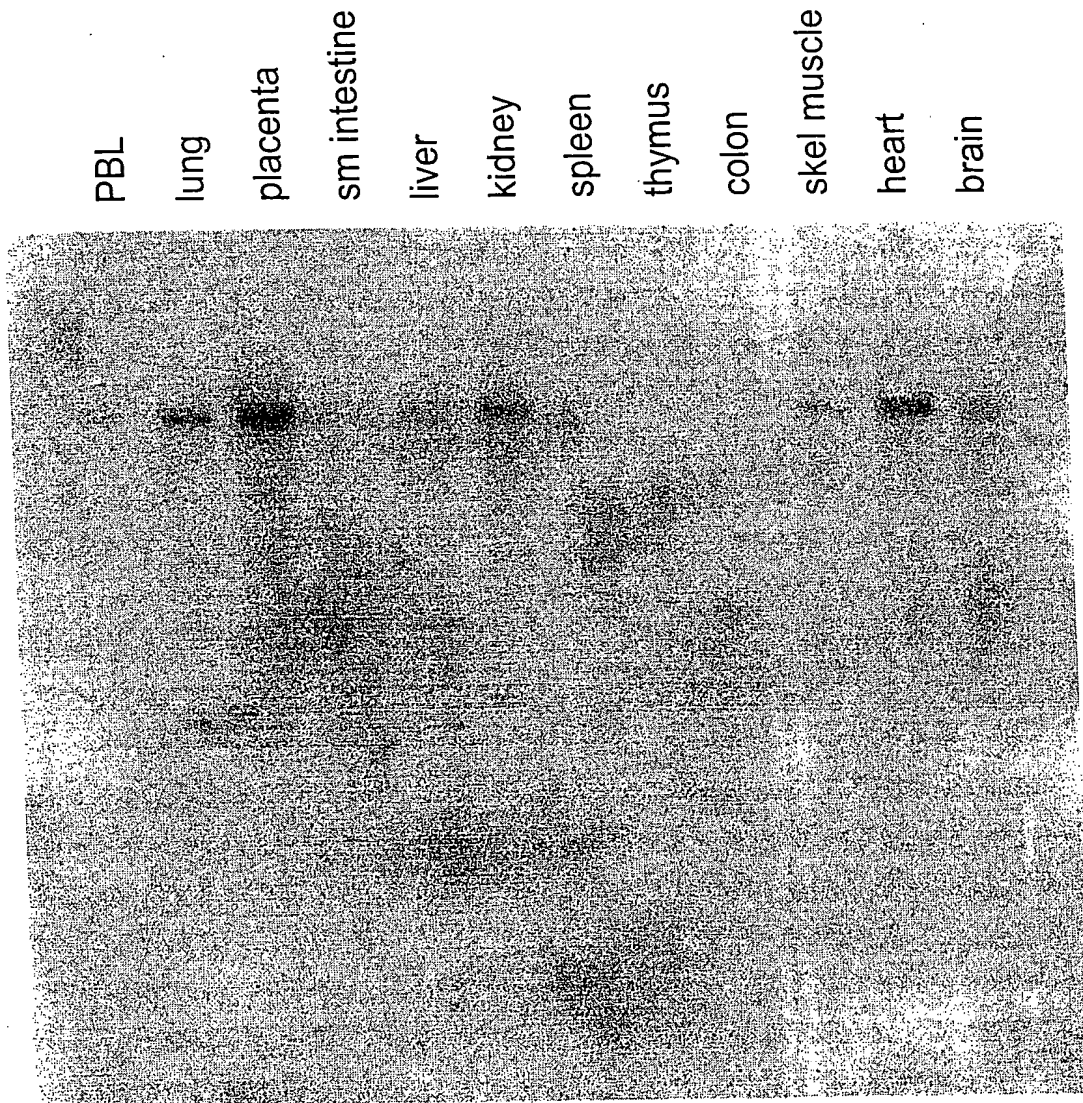


FIG. 4A

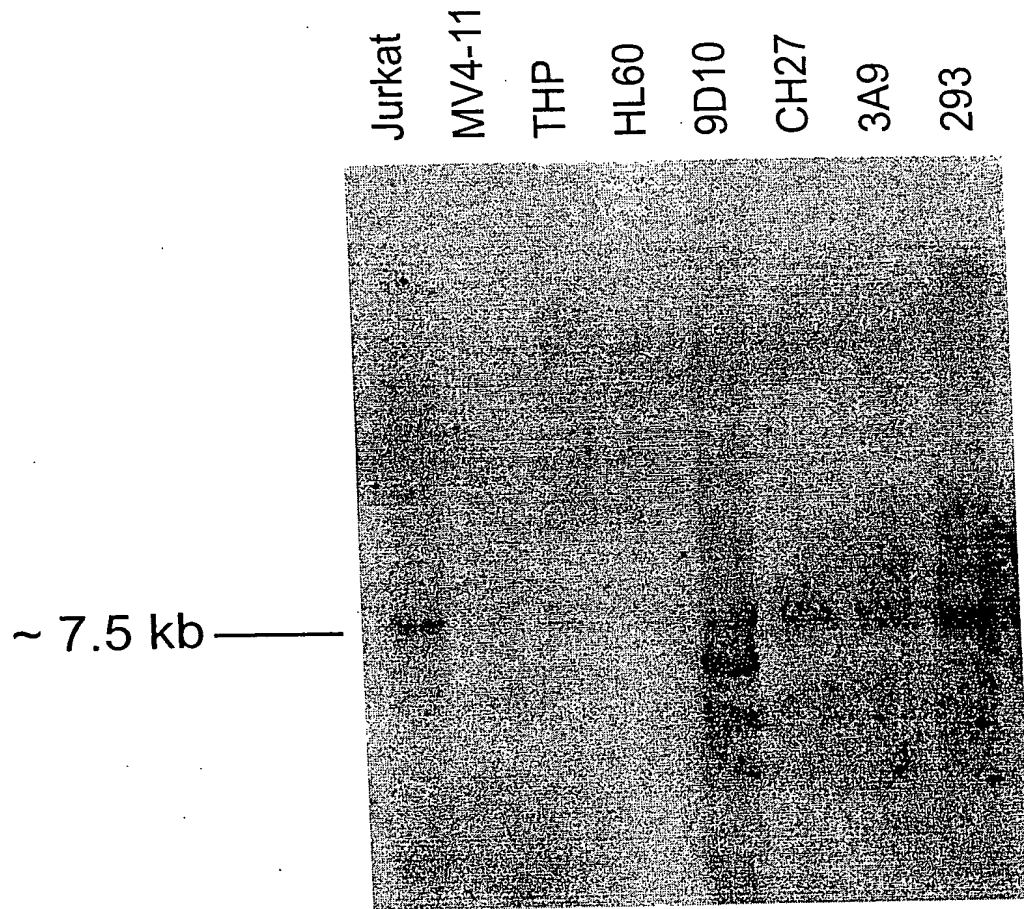


FIG. 4B

HC2A	-----
KIAA	ASGNLDKNARFSAIYRQDSNKLSDNDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----
KIAA	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQ
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----VLHHHQNPFEFYDEIK
KIAA	KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVETRSAFAAVLHHHQNPFEFYDEIK
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	IELPTQLHEKHHLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
KIAA	IELPTQLHEKHHLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
KIAA	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
rat	-----
HC4	-----
HC1	-----
HC3	-----GPGPARSTVSISLISNSARV
HC5	-----
HC2A	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat	-----
HC4	-----MEIQVLIREFLSVIILMQLFWVLPNMIHEDDVPISCPMV
HC1	-----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3	NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSPSPSAES
HC5	-----

FIG.5A

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HC2A	I IHVVAQCHEEGLESHLSYVVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN
KIAA	I IHVVAQCHEEGLESHLSYVVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN
rat	-----
HC4	LFHIVSKCHEEGLD SYLSSFIKYSFRPGKPSAPQAPLIHETLATMMIALLKQSADFLAIN
HC1	LPDIVAKCHEEQLDHSVQSYIKFVFKTR---ACKERPVEDLAKNVTGLLK-SNDSPTVK
HC3	TQAMDRSCNRMSHTETSSFLQTLTGRLP----TKKLFHEELALQWVVCSG--SVR---E
HC5	-----
	Cadherin
	Cleavage
HC2A	KLLRYSWFFFDVLIK SMAQH LIENSKVKLI RNQRF PASYHHAAETVVNMLMPHITQKFGD
KIAA	KLLKYSWFFFDVLIK SMAQH LIENSKVKLI RNQRF PASYHHAVETVVNMLMPHITQKFRD
rat	-----
HC4	KLLKYSWFFFEIIAKSMATYLL ENKIKLTHGQRF PKAYHHALHSLFLAIT-IVESQYAE
HC1	HVLKHSWFFFAIILKSMAQH LIDTNKIQLRPFPE SYQNELDNLMVLSHDHVIWKYKD
HC3	SALQQAWFFFEIMVKSMVHHLYFNDKLEAHRKSRFPERFMDIAALVSTIASDIVSRFQK
HC5	-----
HC2A	NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL
KIAA	NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL
rat	-----
HC4	IPKESRNVNYSLASFLKCCLTLMDRGFVFNLIN---DYIS--GFSPKDPKVLAEYKFEFL
HC1	ALEETRATHSVAREFLKRCFTFMDRGCVFKMVN---NYIS--MFSSGDLKTLQYKFDL
HC3	DTEMVERLNTSLAFFLNDLLSVMDRGFVFSLIKSCYQVSSKLYSLPNPSVLVSLRLDFL
HC5	-----
HC2A	RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL---DYSLTDEF
KIAA	RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL---DYSLTDEF
rat	-----
HC4	QTICNHEHYIPLNLPM-----AFAPKPLQR-----VQDSNL---EYSLSDEY
HC1	QEVQCHEHFIPCLPIRSANIPDPLTPSES-----TQELHASDMPEYSVTNEF
HC3	RIICSHHYVTLNLPCSLTPPASPSVSSATSQSSGFSTNVQDQKIANMFELS--VPF
HC5	-----MNADTAPTSPCPSIS---SQNSSSCSSFQDQKIASMFDRTSRVPA
HC2A	CRNHFLVGLLLREVGTALQEFRE---VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
KIAA	CRNHFLVGLLLREVGTALQEFRE---VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
rat	-----
HC4	CKHHFLVGLLLRETSIALQDNYE---IRYTAISVIKNLLIKHAFDTRYQHKNQQAIAQ
HC1	CRKHFLIGILLREVGFALQEDQD---VRHLALAVLKNLMAKHSFDDRYREPRKQAQIAS
HC3	RQQHYLAGLVLTAVILDPDAEGLFGLHKKVINMVHNLSSHSDSDPRYSDPQIKARVAM
HC5	SSTS-SPGLLFTELAAALDAEGEGISEVQRKAVSAIHSLLSSHDLDPRCVKPEVKVKIAA
HC2A	LYLPLFGLLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
KIAA	LYLPLFGLLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
rat	-----
HC4	LYLFPVGLLL ENIQRLAGRD TLYSCAAMPNSASRDEFPCG-----FTSP--AN--RGSLS
HC1	LYMPLYGMLLDNMPRIYKLDLYPFTVNTSNQGSRDDLTSTNGGFQSQTAKHANSVDTSFS
HC3	LYLPLIGIIMETVPQLYDFTETHNQRGRPICIAATDDYESE-----SG---SMIS
HC5	LYLPLVGIILDALPQLCDFTVADTRRYR---TSGSDEEQE-----GA---GAIT
HC2A	KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQOSS
KIAA	KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQOSS
rat	-----
HC4	TDKDTAYGSFQNG-----HGIKREDSRGLIP-EGATGFDPQNGTGEN-----TRQS
HC1	KDVLNSIAAFSS-----IAISTVNHADSRASLSDSNPSTNEKSSEKTDNCEKIPRPL
HC3	QTVAMAIAGTSVPQ-----LTREGSFLITSTSGRQHT-----
HC5	QNVALAIAGNNFN-----LKTSG-IVLSSLPYKQYN-----

FIG. 5A (cont.)

HC2A	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL
KIAA	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL
rat	-----
HC4	STRSSVSQYNRLDQYEIRSLIMCYLYIVKMI SEDTLLTYWN-KVSPQELINILILLEVCL
HC1	ALIGSTLRFDRLDQAE TRSLLMCFLHIMKTISYETLIAYWQ-RAPSPEVSDFFSILDVCL
HC3	-----TFSAESRSLLICLLWVLKN-ADETVLQKWFTDLSVLQLNRLDLLLYLCV
HC5	-----MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV
HC2A	HQFQYMCKRYIARNQEGLG--PIVHDRKS-----QTFVSRNRTGMM
KIAA	HQFQYMCKRYIAR-----TGMM
rat	-----
HC4	FHFRYMGKRNIARVHDAWLSKHFGIDRKS-----QTMPALNRNRSGVM
HC1	QNFYLGKRNIIRKIAAAF--KFVQSTQNNGTILKGSNPSCQTSGLLAQWMHSTSRHEGHC
HC3	SCFEYKGKVFERMNSLTFK--KSKDMRAK-----LEEAILGSIGARQEMV
HC5	LCFEYKGKQSSDKVSTQVLQ--KSRDVKAR-----LEEALLRGE GARGEMM
HC2A	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
KIAA	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
rat	-----
HC4	QARLQHL-----SSLESS-----FTLNHSSTTTEADIFHQALLEGNTATEVS
HC1	QHRSTLPIIRGK---NALSNEPKL---LQMLDNTMTSNEIDIVHHVDTEANIATEGC
HC3	RRSRGQLERSPSGSAFGSQENLRWRKDMTHWRQNTKLDKSRAEIEHEALIDGNLATEAN
HC5	RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAEILDQEALISGNLATEAH
HC2A	LTALDTLSLFTLAFKNQLLADHGHNPIMKKVFDVYLCFLQKHQSE TALKNVFTALRS LIY
KIAA	LTALDTLSLFTLAFKNQLLADHGHNPIMKKVFDVYLCFLQKHQSE TALKNVFTALRS LIY
rat	-----KLSRGHSPIMKKVFDVYLCFLQKHQSE MALKNVFTALRS LIY
HC4	LTVLDTISFFTQCFKTHFLNNDGHNPLMKKVFEDIHLAFLKNGQSEVSLKHVFASIRAFIS
HC1	LTILDVLSLFTQTHQRQLQQCDCQNSLMKRGFDTYMLFFQVNSATALKHVFASIRLRFVC
HC3	LIILDTLEIVVQTVS--VTES--KESILGGVLKVLHSMACNQSAVYLQHC FATQALVS
HC5	LIILDMQENIQASS--ALDC--KDSLLGGVLRVLVNSLNCDSQSTTYLTHCFATLRALIA
HC2A	KFPSTFYEGRADMC AALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTH
KIAA	KFPSTFYEGRADMC AALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTH
rat	KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTH
HC4	KFPSAFFKGRVNMCAAFCEYVLKCCTSKISSSTRNEASALLYLLMRNNFEYTKRKTFLRTH
HC1	KFPSAFFQGPADLCGSFCYEVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSH
HC3	KFPELLFEEETEQCADLCRLRLRHCS SIGTIRSHPSASLYLLMRQNF EIGN--N FARVK
HC5	KFGDLLFEEVEQCFDLCHQVLHHCSSSMDVTRSQCATLYLLMRFSFGATS--N FARVK
HC2A	LQVII SVS QLIADVVGIGETR FQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRIRTVLM
KIAA	LQVII SVS QLIADVVGIGETR FQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRIRTVLM
rat	LQVII SLSQLIADVVGIGETR FQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRIRTVLM
HC4	LQIIIAVS QLIADVALSGGSRFQESLFI INNFANS DRPMLARAFPAEVKDLTKRIRTVLM
HC1	LQLIKAVS QLIAD-AGIGGSRFQHS LAITNNFANGDKQMKNSNFP AEV KDLTKRIRTVLM
HC3	MQVPMSLSSLVGTSQNFNEEFLRRSLKTILTYAEEDLELRETTFPDQVQDLVFNLHMILS
HC5	MQVTMSLASILVGRAPDFNEEHLRRSLR TILAYSEEDTAMQMT PFP TQVEELL CNLNSILY

FIG. 5A (cont.)

Transmembrane

HC2A	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKN	DLSEAAMCYVHV
KIAA	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKN	DLSEAAMCYVHV
rat	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKN	DLSEAAMCYVHV
HC4	ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKTWLD SMAKIHVKN	DFSEAAMCYVHV
HC1	ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLE SMAKIHARNG	DLSEAAMCYIHI
HC3	DTVQMKEHQEDPEMLIDLMYRIAKGYQTS PDLRLTWLQNMAGKHSERSN	HAEAAQCLVHS
HC5	DTVQMREFQEDPEMLMDIMYRIAKSYQAS PDLRLTWLQNMAGKHTKKKCY	TEAAMCLVHA

		SH3	
HC2A	TALVAEYI	TRKGV-----	FRQGCTAFRVITPN
KIAA	TALVAEYI	TRKEA-----	VQWEPPLLPHSHSACLRRSRGGVFRQGCTAFRVITPN
rat	TALVAEYI	TRKEAD-----	LALQREPPVFPYSHTSCQRKSRGGMFRQGCTAFRVITPN
HC4	AALVAEYI	HRKKL-----	FPNGCSAFKKITPN
HC1	AALIAEYI	KRKGWYKVEKIC	TASLLSEDTHPCDNSLLTTPSGGSMFSGWPAFLSITPN
HC3	AALVAEYI	SMLD-----	RKYLPGVCVTFQNISSN
HC5	AALVAEYI	SMLD-----	HSYLPVGSVSFQNISSN

HC2A	IDEEASMMEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIIP
KIAA	IDEEASMMEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIIP
rat	IDEEASMMEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAERLRAGLLTSINSSSP
HC4	IDEEGAMKEDAGMMD-----	VHYSEEVLLLELLEQCVNGLWKAERYEIISEISKLIGPI
HC1	IKKEGAAKEDSGMHD-----	TPYNENILVEQLYMCGEFLWKSEYELIADVKNPIIAV
HC3	VLEESAVSDDVSPDEEGICSGKYFTESGLVGLLEQAAASF	SMAGMYEAVNEVYKVLIP
HC5	VLEESVVSSEDTLSPDEGDGVCAGQYFTESGLVGLLEQAAELF	STGGLYETVNEVYKVLIP

		ITAM	ITAM	ITAM	ITAM
HC2A	YEKRRD-----				
KIAA	YEKRRDFERLAHLIDTLH	RAYSKVTEVMHSGRLLG	TYFRVAFFGQAAQYQFTDSETDVE		
rat	SMKSGGTLETHLYDTLH	RPYSKVTEVITR-----	A-----	AGSWDLLPGGLFGQ	
HC4	YENRREFENLTQVYRTLH	GAYTKILEVMHTKKRLLG-----		TFFRVAFYFGQ	
HC1	FEKQRDFKKLSDLIYDIH	RSYLVKVAEVVNSEKRLFG-----		RYRVAFYFGQ	
HC3	HEANRDAKKLSTIHGKLQ	EAFSKIYHQSTGWERMFG-----		TYFRVGFYFG-	
HC5	LEAHREFRKLTLTHSKLQ	RAFDSTVNKDH--KRMFG-----		TYFRVGFYFG-	

		ITAM	ITAM
HC2A	-FFEDEDGKEYIYKEPKLTPLSEISQRLKLYSDKFGSENVKMIQDSGKVNPKDLD	SKYA	
KIAA	GFFEDEDGKEYIYKEPKLTPLSEISQRLKLYSDKFGSENVKMIQDSGKVNPKDLD	SKYA	
rat	GFFEDEDGKEYIYKEPKLTPLSEISQRLKLYSDKFGSENVKMIQDSGKVNPKDLD	SKFA	
HC4	SFFEEDDGKEYIYKEPKLTGLSEISLRVLVLYGKFGTENVKIIQDSKVNKAKELD	PKYA	
HC1	GFFEEEDGKEYIYKEPKLTGLSEISQRLKLYADKFGADNVKIIQDSNVKVNPKDLD	PKYA	
HC3	TKFGDLDEQEFVYKEPAITKLAIEISHRLEGFYGERFGEDVVEVIKDSNPVDKCKLD	PNKA	
HC5	SKFGDLDEQEFVYKEPAITKLPEISHRLEAFYGCFCGAEFVEVIKDSNPVDKCKLD	PNKA	

		ITAM
HC2A	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVVEEQKRR	TILTA
KIAA	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVVEEQKRR	TILTA
rat	YIQVTHVIPFFDEKELQERKTEFERCHNIRRFMFEMPFTQTGKRQGGVVEEQKRR	TILTA
HC4	HIQVTVVKPYFDDKELTERKTEFERNHNISRFVFEAPYTLGKKQGGCIEEQKRR	TILT
HC1	YIQVTVVTPFFEEKEIEDRKTDFFEMHHNINRFVFETPFTLSGKKHGGVAEQKRR	TILT
HC3	YIQITVVEPYFDTYEMKDRITYFDKNYNLRREMYCTPFTLDGRAHGEHQFRRK	TILT
HC5	YIQITVVEPYFDTYEMKDRITYFEKNFNLRREMYCTPFTLEGRPRGELHEQYRR	NTVLTT

FIG. 5A (cont.)

		Coiled-Coil 1
HC2A	IHC	FPYVKKRIPVMYQHHTDINPIEVAIDEMSKKVAELRQLCSSAEVDMIKLQKLQGSV
KIAA	IHC	FPYVKKRIPVMYQHHTDINPIEVAIDEMSKKVAELRQLCSSAEVDMIKLQKLQGSV
rat	IHC	FPYVKKRIPVMYQHHTDINPIEVAIDEMSKKVAELHQLCSSAEVDMIKLQKLQGSV
HC4	SNS	FPYVKKRIPINCEQQINIKPIDGATDEIKDKTAEIQKLCSSSTDVDMIQKLQKLQGSV
HC1	SHL	FPYVKKRIQVISQSSTEINPIEVAIDEMSRKVSELNQLCTMEEVDMISLQKLQGSV
HC3	SHAF	PYIKTRVNVTHKEEIIITPIEVAIDEMQKKTQELAFATHQDPADPKMLQMLQGSV
HC5	MHAF	PYIKTRISVIQKEEFVITPIEVAIDEMKKKTLQLAVAINQEPDAKMLQMLQGSV
		Coiled-Coil 2
HC2A	SVQ	VNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
KIAA	SVQ	VNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
rat	SVQ	VNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
HC4	SVQ	VNAGPLAYARAFLLDSQASKYPKKVSELKDMFRKFIQACSIALAVNERLIKEDQVE
HC1	SVK	VNAGPMAYARAFLEETNAKKYPDNQVKLLKEIFRQFADACGQALAVNERLIKEDQLE
HC3	GTT	VNQGPLEVAQVFLSEIPSDPKLFRHHNKLRLCFKDFTKRCEDALRNKSLIGPVQKE
HC5	GAT	VNQGPLEVAQVFLAEIPADPKLYRHHNKLRLCFKEFIMRCGEAVEKNKRLITADQRE
		Coiled-Coil 2
HC2A	YQE	EMKANYREMAKELSEIMHEQICPLEEKTS-VLPNSLHIFNAISGTPSTMVHGMTSS
KIAA	YQE	EMKANYREMAKELSEIMHEQLG-----
rat	YQE	EMKANYREIRKELSDIIVPRICPGEDKRATKFAHLQRHQRTDNKHSGSRVDQFILS
HC4	YHE	GLKSNFRDMVKELSDIIEHQILQEDTMHSPWMSNTLHVFCASGTSSDRGYGSPRYA
HC1	YQE	ELRSHYKDMSELSTVMNEQITGRDDLK---RGVDQCTRVISKATPALPTVSISS
HC3	YQRE	LG---KLSS---PZ-----
HC5	YQEL	KKNYNKLNENLRPMIERKIPELYKPIFRVESQKRD SFHRSSFRKCETQLSQGSZ-
		PBM
HC2A	SSVV	-----
KIAA	SSVV	-----
rat	CVT	LPHEPHVGTCTFVMCKLRTTFRANHWFCQAQEEAMGNGREKEPWTVIFNSRFYRSWGK
HC4	EV	-----
HC1	SAEV	-----
HC3	-----	-----
HC5	-----	-----
HC2A	-----	-----
KIAA	-----	-----
rat	VHIF	-----
HC4	-----	-----
HC1	-----	-----
HC3	-----	-----
HC5	-----	-----

FIG. 5A (cont.)

	A	B	
CLASP-1	YRVAFYGQ:::::::::::::GFFEEEEGKEYIYKEP		
KIAA1058	FRVAFFGQAAQYQFTDSETDVEGFFEDEDGKEYIYKEP		
CLASP-2		FEDEDGKEYIYKEP	
CLASP-6	FRVAFFGQ:::::::::::::GFFEDEDGKEYIYKEP		
CLASP-4	FRVAFYGQ:::::::::::::SFFEDEDGKEYIYKEP		
DOCK180	FAVGYYGQ:::::::::GFPTFLRGKVFIYRGKEYERRED		
DOCK2	FAVGYYGQ:::::::::GFPSFLRNKVFIYRGKEYERRED		
DOCK3	FRVGFIYGR:::::::::::::KFPFFLRNKEYVCRGH		
KIAA0716	FRVGFIYGK:::::::::::::KFPFFLRNKEFVCRGH		
CLASP-3	FRVGFIYGT:::::::::::::KFGDLDEQEFVYKEP		
CONSENSUS	F V FYG	KEY K	
	YF	Q F R	
			C
TRG	<u>PKLTPLSEISQRLCLKLYSDKFGSENVKMIQDSGKVNPKDLDSKEFYIQVTHVTPFFDEKE</u>		
CLASP-1	PKLTGLSEISQRLCLKLYADKFGADNVKIIQDSNVNPKDLDPKYAYIQVTYVTPFFEEKE		
CLASP-2	PKLTPLSEISQRLCLKLYSDKFGSENVKMTQDSGKVNPKDLDSKYAYIQVTHVIPFFDEKE		
CLASP-4	PKLTGLSEISLRLVKLYGEKFGTENVKIIQDSKVNAKELDPKYAHIQVTYVKPYFDDKE		
CLASP-3	PAITKLAEISHRLEGFYGERFGEDVVEVIKDSNPVDKCKLDPNKAYIQITYVEPYFDTYE		
KIAA0716	HDYERLEAFQQRMLNEFPFAIA-----MQHANQPDETIFQAEAQYLQIYAVTPIPEEQE		
DOCK3	HDYERLEAFQQRMLSEFPQAVA-----MQHPNHPDDAILQCDAAQYLQIYAVTPIPDYVD		
DOCK2	FQMQLMTQFPNAEK-----MNTTSAPGDDVKNAPGOYIQCFTVQPVLEHP		
DOCK180	EYERREDFQMQLMTQFPNAEK-----MNTTSAPGDDVKNAPGOYIQCFTVQPVLEHP		
CONSENSUS	L	L Y	YIQ+ V P D
		M F	L E
	D	E	
CLASP-1	RTILTTSHLFPYVKKRIQVISQSSTELNPIEVAIDEMSRKVSELN		
TRG	RTILTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELH		
KIAA1058	RTILTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELR		
CLASP-2	RTILTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELR		
CLASP-6	RTILTAIHCFPYVKKRIPVMYQHHTDLNPIEV:HDEMSSKKVAELR		
CLASP-4	RTILTTSNSFPYVKKRIPINCEQQINLKPIDVATDEIKDKTAELO		
CLASP-3	KTILTTSHAFPIYKTRVNVTHKEEIIILTPIEVAIEDMOKKTQELA		
CLASP-5	NTVLTTMHAFPIYKTRISVIQKEEFVLTPIEVAIEDMOKKTLQLA		
KIAA0716	RTSLYLVSPLPGISRWFVEVEKREVVMSPLENAIEVLENKNQOLK		
DOCK2	RTSFVTAYKLPGLRWFEVHMSQTTISPLENAIETMSTANEKIL		
DOCK3	RTTLTLTHSLPGISRWFVEVERRELVEVSPLENAIQVVENKNQELR		
DOCK180	RTSFVTAYKLPGLRWFEVHMSQTTISPLENAIETMSTANEKIL		
CONSENSUS	RT L	FP V + V + P+E AI+ M +L	
	F	L L	I

FIG. 5B

	F				G			
CLASP-1	SLQLKLQGSVSVKVNAGPMA Y ARAFLEETNAKKY P DNQV--KLLKEIFRQFADACGQALD							
TRG	<u>KLQLKLQGSVSVQVNAGPLAYARAF</u> <u>LDDTNTKRY</u> <u>EDNKV--KILKEVFRQFVEACGQALA</u>							
KIAA1058	KLQLKLQGSVSVQVNAGPLAYARAF <u>LDDTNTKRY</u> <u>EDNKV--KILKEVFRQFVEACGQALA</u>							
CLASP-2	KLQLKLQGSVSVQVNAGPLAYARAF <u>LDDTNTKRY</u> <u>EDNKV--KILKEVFRQFVEACGQALA</u>							
CLASP-6	KLQLKLQGSVSVQVNAGPLAYARAF <u>LDDTNTKRY</u> <u>EDNKV--KILKEVFRQFVEACGQALA</u>							
CLASP-3	MLQMVLQGSVGTTVNQGPLEVAQVFLSE--IPSD E KLFRHHNKLRLCFKDFTKRCEDALR							
CLASP-4	QLQLKLQGCVSVQVNAGPLAYARAF <u>LND</u> SQASKY E PKKVSELKDMFRKFI--QACSI A LE							
CLASP-5	MLQMVLQGSVGATVNQGPLEVAQVFLAE--IPAD E KLYRHHNKLRLCFKEFIMRCGEAVE							
KIAA0716	PLTMCLNGVIDAAVNGGVSR Y QEAFVKEYILSH E DGEK I ARLRELML E QAQILEFGLA							
DOCK2	PLSMLLNGIVDPAVMG G FAKYEKAFFTEEYVRD H EDQDKLTH L KDLIAWQIPFLGAGIK							
DOCK3	LLSMCLNGVIDAAVNGGI A RYQEAFDDKDYINKH E GDAEKITQLKELMQEQVHVLGVGLA							
DOCK180	PLSMLLNGIVDPAVMG G FAKYEKAFFTEEYVRD H EAHEKIEKLKDLIAWQIPFLAEGIR							
CONSENSUS	L	M	L+G	V	VN	G	Y	AFL + + E L+ L
				I			V	V F + I

DOCK2=KIAA0209

DOCK3=KIAA0299

CLASP2variant=KIAA1058

FIG. 5B (cont.)

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1
A

2 32
GTT TTA CAC CAT CAC CAA AAC CCA GAA TTT TAT GAT GAG ATT AAA ATA GAG TTG CCC ACT
val leu his his his gln asn pro glu phe tyr asp glu ile lys ile glu leu pro thr


62 92
CAG CTG CAT GAA AAG CAC CAC CTG TTG CTC ACA TTC TTC CAT GTC AGC TGT GAC AAC TCA
gln leu his glu lys his his leu leu leu thr phe phe his val ser cys asp asn ser

122 152
AGT AAA GGA AGC ACG AAG AAG AGG GAT GTC GTT GAA ACC CAA GTT GGC TAC TCC TGG CTT
ser lys gly ser thr lys lys arg asp val val glu thr gln val gly tyr ser trp leu

182 212
CCC CTC CTG AAA GAC GGA AGG GTG GTG ACA AGC GAG CAG CAC ATC CCG GTC TCG GCG AAC
pro leu leu lys asp gly arg val val thr ser glu gln his ile pro val ser ala asn

242 272
CTT CCT TCG GGC TAT CTT GGC TAC CAA GAG CTT GGG ATG GGC AGG CAT TAT GGT CCG GAA
leu pro ser gly tyr leu gly tyr gln glu leu gly met gly arg his tyr gly pro glu

302 332
ATT AAA TGG GTA GAT GGA GGC AAG CCA CTG CTG AAA ATT TCC ACT CAT CTG GTT TCT ACA
ile lys trp val asp gly gly lys pro leu leu lys ile ser thr his leu val ser thr
ref 1.1, 1.2 and 1.3

362 392
GTG TAT ACT CAG  GAT CAG CAT TTA CAT AAT TTT TTC CAG TAC TGT CAG AAA ACC GAA TCT
val tyr thr gln asp gln his leu his asn phe phe gln tyr cys gln lys thr glu ser

422 452
GGA GCC CAA GCC TTA GGA AAC GAA CTT GTA AAG TAC CTT AAG AGT CTG CAT GCG ATG GAA
gly ala gln ala leu gly asn glu leu val lys tyr leu lys ser leu his ala met glu

482 512
GGC CAC GTG ATG ATC GCC TTC TTG CCC ACT ATC CTA AAC CAG CTG TTC CGA GTC CTC ACC
gly his val met ile ala phe leu pro thr ile leu asn gln leu phe arg val leu thr

542 572
AGA GCC ACA CAG GAA GAA GTC GCG GTT AAC GTG ACT CGG GTC ATT ATT CAT GTG GTT GCC
arg ala thr gln glu glu val ala val asn val thr arg val ile ile his val val ala

602 632
CAG TGC CAT GAG GAA GGA TTG GAG AGC CAC TTG AGG TCA TAT GTT AAG TAC GCG TAT AAG
gln cys his glu glu gly leu glu ser his leu arg ser tyr val lys tyr ala tyr lys

662 692
GCT GAG CCA TAT GTT GCC TCT GAA TAC AAG ACA GTG CAT GAA GAA CTG ACC AAA TCC ATG
ala glu pro tyr val ala ser glu tyr lys thr val his glu glu leu thr lys ser met

FIG. 6A

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722		752
ACC ACG ATT CTC AAG CCT TCT GCC GAT TTC CTC ACC AGC AAC AAA CTA CTG AGG TAC TCA		
thr thr ile leu lys pro ser ala asp phe leu thr ser asn lys leu leu arg tyr ser		
782		812
TGG TTT TTC TTT GAT GTA CTG ATC AAA TCT ATG GCT CAG CAT TTG ATA GAG AAC TCC AAA		
trp phe phe phe asp val leu ile lys ser met ala gln his leu ile glu asn ser lys		
842	Cadherin Cleavage	872
GTT AAG TTG CTG CGA AAC CAG AGA TTT CCT GCA TCC TAT CAT CAT GCA GCG GAA ACC GTT		
val lys leu leu arg asn gln arg phe pro ala ser tyr his his ala ala glu thr val		
902		932
GTA AAT ATG CTG ATG CCA CAC ATC ACT CAG AAG TTT GGA GAT AAT CCA GAG GCA TCT AAG		
val asn met leu met pro his ile thr gln lys phe gly asp asn pro glu ala ser lys		
962		992
AAC GCG AAT CAT AGC CTT GCT GTC TTC ATC AAG AGA TGT TTC ACC TTC ATG GAC AGG GGC		
asn ala asn his ser leu ala val phe ile lys arg cys phe thr phe met asp arg gly		
		ref 2.1
1022		1052
TTT GTC TTC AAG CAG ATC AAC AAC TAC ATT AGC TGT TTT GCT CCT GGA GAC CCA AAG ACC		
phe val phe lys gln ile asn asn tyr ile ser cys phe ala pro gly asp pro lys thr		
1082		1112
CTC TTT GAA TAC AAG TTT GAA TTT CTC CGT GTA GTG TGC AAC CAT GAA CAT TAT ATT CCG		
leu phe glu tyr lys phe glu phe leu arg val val cys asn his glu his tyr ile pro		
1142		1172
TTG AAC TTA CCA ATG CCA TTT GGA AAA GGC AGG ATT CAA AGA TAC CAA GAC CTC CAG CTT		
leu asn leu pro met pro phe gly lys gly arg ile gln arg tyr gln asp leu gln leu		
1202		1232
GAC TAC TCA TTA ACA GAT GAG TTC TGC AGA AAC CAC TTC TTG GTG GGA CTG TTA CTG AGG		
asp tyr ser leu thr asp glu phe cys arg asn his phe leu val gly leu leu leu arg		
1262		1292
GAG GTG GGG ACA GCC CTC CAG GAG TTC CGG GAG GTC CGT CTG ATC GCC ATC AGT GTG CTC		
glu val gly thr ala leu gln glu phe arg glu val arg leu ile ala ile ser val leu		
		ref 3.1
1322		1352
AAG AAC CTG CTG ATA AAG CAT TCT TTT GAT GAC AGA TAT GCT TCA AGG AGC CAT CAG GCA		
lys asn leu leu ile lys his ser phe asp asp arg tyr ala ser arg ser his gln ala		
1382		1412/471
AGG ATA GCC ACC CTC TAC CTG CCT CTG TTT GGT CTG CTG ATT GAA AAC GTC CAG CGG ATC		
arg ile ala thr leu tyr leu pro leu phe gly leu leu ile glu asn val gln arg ile		
1442		1472
AAT GTG AGG GAT GTG TCA CCC TTC CCT GTG AAC GCG GGC ATG ACC GTG AAG GAT GAA TCC		
asn val arg asp val ser pro phe pro val asn ala gly met thr val lys asp glu ser		

FIG. 6A (cont.)

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1502 1532
CTG GCT CTA CCA GCT GTG AAT CCG CTG GTG ACG CCG CAG AAG GGA AGC ACC CTG GAC AAC
leu ala leu pro ala val asn pro leu val thr pro gln lys gly ser thr leu asp asn
ref 4.1 and 4.2

1562 1592
AGC CTG CAC AAG GAC CTG CTG GGC GCC ATC TCC GGC ATT GCT TCT CCA TAT ACA ACC TCA
ser leu his lys asp leu leu gly ala ile ser gly ile ala ser pro tyr thr thr ser

1622 1652
ACT CCA AAC ATC AAC AGT GTG AGA AAT GCT GAT TCG AGA GGA TCT CTC ATA AGC ACA GAT
thr pro asn ile asn ser val arg asn ala asp ser arg gly ser leu ile ser thr asp
ref 5.1 and 5.2

1682 1712
TCG GGT AAC AGC CTT CCA GAA AGG AAT AGT GAG AAG AGC AAT TCC CTG GAT AAG CAC CAA
ser gly asn ser leu pro glu arg asn ser glu lys ser asn ser leu asp lys his gln

1742 1772
CAA AGT AGC ACA TTG GGA AAT TCC GTG GTT CGC TGT GAT AAA CTT GAC CAG TCT GAG ATT
gln ser ser thr leu gly asn ser val val arg cys asp lys leu asp gln ser glu ile

1802 1832
AAG AGC CTA CTG ATG TGT TTC CTC TAC ATC TTA AAG AGC ATG TCT GAT GAT GCT TTG TTT
lys ser leu leu met cys phe leu tyr ile leu lys ser met ser asp asp ala leu phe

1862 1892
ACA TAT TGG AAC AAG GCT TCA ACA TCT GAA CTT ATG GAT TTT TTT ACA ATA TCT GAA GTC
thr tyr trp asn lys ala ser thr ser glu leu met asp phe phe thr ile ser glu val
ref 6.1

1922 1952
TGC CTG CAC CAG TTC CAG TAC ATG GGG AAG CGA TAC ATA GCC AGG AAC CAG GAG GGG TTG
cys leu his gln phe gln tyr met gly lys arg tyr ile ala arg asn gln glu gly leu

1982 2012
GGA CCC ATA GTT CAT GAT CGA AAG TCT CAG ACA TTG CCT GTT TCC CGT AAC AGA ACA GGA
gly pro ile val his asp arg lys ser gln thr leu pro val ser arg asn arg thr gly

2042 2072
ATG ATG CAT GCC AGA TTG CAG CAG CTG GGC AGC CTG GAT AAC TCT CTC ACT TTT AAC CAC
met met his ala arg leu gln gln leu gly ser leu asp asn ser leu thr phe asn his

2102 2132
AGC TAT GGC CAC TCG GAC GCA GAT GTT CTG CAC CAG TCA TTA CTT GAA GCC AAC ATT GCT
ser tyr gly his ser asp ala asp val leu his gln ser leu leu glu ala asn ile ala
ref 7.1

2162 2192
ACT GAG GTT TGC CTG ACA GCT CTG GAC ACG CTT TCT CTA TTT ACA TTG GCG TTT AAG AAC
thr glu val cys leu thr ala leu asp thr leu ser leu phe thr leu ala phe lys asn

2222 2252
CAG CTC CTG GCC GAC CAT GGA CAT AAT CCT CTC ATG AAA AAA GTT TTT GAT GTC TAC CTG
gln leu leu ala asp his gly his asn pro leu met lys lys val phe asp val tyr leu

2282 2312

FIG. 6A (cont.)

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TGT TTT CTT CAA AAA CAT CAG TCT GAA ACG GCT TTA AAA AAT GTC TTC ACT GCC TTA AGG
cys phe leu gln lys his gln ser glu thr ala leu lys asn val phe thr ala leu arg

2342 2372
TCC TTA ATT TAT AAG TTT CCC TCA ACA TTC TAT GAA GGG AGA GCG GAC ATG TGT GCG GCT
ser leu ile tyr lys phe pro ser thr phe tyr glu gly arg ala asp met cys ala ala

2402 2432
CTG TGT TAC GAG ATT CTC AAG TGC TGT AAC TCC AAG CTG AGC TCC ATC AGG ACG GAG GCC
leu cys tyr glu ile leu lys cys cys asn ser lys leu ser ser ile arg thr glu ala

2462 2492
TCC CAG CTG CTC TAC TTC CTG ATG AGG AAC AAC TTT GAT TAC ACT GGA AAG AAG TCC TTT
ser gln leu leu tyr phe leu met arg asn asn phe asp tyr thr gly lys lys ser phe

2522 2552
GTC CGG ACA CAT TTG CAA GTC ATC ATA TCT GTC AGC CAG CTG ATA GCA GAC GTT GTT GGC
val arg thr his leu gln val ile ile ser val ser gln leu ile ala asp val val gly

2582 2612
ATT GGG GAA ACC AGA TTC CAG CAG TCC CTG TCC ATC ATC AAC AAC TGT GCC AAC AGT GAC
ile gly glu thr arg phe gln gln ser leu ser ile ile asn asn cys ala asn ser asp

2642 2672
CGG CTT ATT AAG CAC ACC AGC TTC TCC TCT GAT GTG AAG GAC TTA ACC AAA AGG ATA CGC
arg leu ile lys his thr ser phe ser ser asp val lys asp leu thr lys arg ile arg

2702 2732
ACG GTG CTA ATG GCC ACC GCC CAG ATG AAG GAG CAT GAG AAC GAC CCA GAG ATG CTG GTG
thr val leu met ala thr ala gln met lys glu his glu asn asp pro glu met leu val

2762 2792
GAC CTC CAG TAC AGC CTG GCC AAA TCC TAT GCC AGC ACG CCC GAG CTC AGG AAG ACG TGG
asp leu gln tyr ser leu ala lys ser tyr ala ser thr pro glu leu arg lys thr trp

2822 2852 |XXXXXXXXXXXXXXXXXXXX Predicted
CTC GAC AGC ATG GCC AGG ATC CAT GTC AAA AAT GGC GAT CTC TCA GAG GCA GCA ATG TGC
leu asp ser met ala arg ile his val lys asn gly asp leu ser glu ala ala met cys

Transmembrane Domain XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX|
TAT GTC CAC GTA ACA GCC CTA GTG GCA GAA TAT CTC ACA CGG AAA GGC GTG TTT AGA CAA
tyr val his val thr ala leu val ala glu tyr leu thr arg lys gly val phe arg gln

2942 2972
GGA TGC ACC GCC TTC AGG GTC ATT ACC CCA AAC ATC GAC GAG GAG GCC TCC ATG ATG GAA
gly cys thr ala phe arg val ile thr pro asn ile asp glu glu ala ser met met glu
ref 8.1 ↓

3002 3032
GAC GTG GGG ATG CAG GAT GTC CAT TTC AAC GAG GAT GTG CTG ATG GAG CTC CTT GAG CAG
asp val gly met gln asp val his phe asn glu asp val leu met glu leu leu glu gln

3062 3092
TGC GCA GAT GGA CTC TGG AAA GCC GAG CGC TAC GAG CTC ATC GCC GAC ATC TAC AAA CTT
cys ala asp gly leu trp lys ala glu arg tyr glu leu ile ala asp ile tyr lys leu

FIG. 6A (cont.)

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                                ref 9.1
3122                               3152
ATC ATC CCC ATT TAT GAG AAG CGG AGG GAT TTC TTT GAA GAT GAA GAT GGA AAG GAG TAT
ile ile pro ile tyr glu lys arg arg asp phe phe glu asp glu asp gly lys glu tyr

                                3212
3182                               3212
ATT TAC AAG GAA CCC AAA CTC ACA CCG CTG TCG GAA ATT TCT CAG AGA CTC CTT AAA CTG
ile tyr lys glu pro lys leu thr pro leu ser glu ile ser gln arg leu leu lys leu
                                ref 10.1
3242                               3272
TAC TCG GAT AAA TTT GGT TCT GAA AAT GTC AAA ATG ATA CAG GAT TCT GGC AAG GTC AAC
tyr ser asp lys phe gly ser glu asn val lys met ile gln asp ser gly lys val asn

                                3332
3302                               3332
CCT AAG GAT CTG GAT TCT AAG TAT GCA TAC ATC CAG GTG ACT CAC GTC ATC CCC TTC TTT
pro lys asp leu asp ser lys tyr ala tyr ile gln val thr his val ile pro phe phe

                                3392
3362                               3392
GAC GAA AAA GAG TTG CAA GAA AGG AAA ACA GAG TTT GAG AGA TCC CAC AAC ATC CGC CGC
asp glu lys glu leu gln glu arg lys thr glu phe glu arg ser his asn ile arg arg

                                3452
3422                               3452
TTC ATG TTT GAG ATG CCA TTT ACG CAG ACC GGG AAG AGG CAG GGC GGG GTG GAA GAG CAG
phe met phe glu met pro phe thr gln thr gly lys arg gln gly gly val glu glu gln
                                ref 11.1
3482                               3512
TGC AAA CGG CGC ACC ATC CTG ACA GCC ATA CAC TGC TTC CCT TAT GTG AAG AAG CGC ATC
cys lys arg arg thr ile leu thr ala ile his cys phe pro tyr val lys lys arg ile

                                3572
3542                               3572
CCT GTC ATG TAC CAG CAC CAC ACT GAC CTG AAC CCC ATC GAG GTG GCC ATT GAC GAG ATG
pro val met tyr gln his his thr asp leu asn pro ile glu val ala ile asp glu met

3602 xxxxxxxx Coiled coil 1 cont'd xxx 3632 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
AGT AAG AAG GTG GCG GAG CTC CGG CAG CTG TGC TCC TCG GCC GAG GTG GAC ATG ATC AAA
ser lys lys val ala glu leu arg gln leu cys ser ala glu val asp met ile lys
                                ref 12.1
3662 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx | 3692
CTG CAG CTC AAA CTC CAG GGC AGC GTG AGT GTT CAG GTC AAT GCT GGC CCA CTA GCA TAT
leu gln leu lys leu gln gly ser val ser val gln val asn ala gly pro leu ala tyr

                                3752
3722                               3752
GCG CGA GCT TTC TTA GAT GAT ACA AAC ACA AAG CGA TAT CCT GAC AAT AAA GTG AAG CTG
ala arg ala phe leu asp asp thr asn thr lys arg tyr pro asp asn lys val lys leu

                                3812
3782                               3812
CTT AAG GAA GTT TTC AGG CAA TTT GTG GAA GCT TGC GGT CAA GCC TTA GCG GTA AAC GAA
leu lys glu val phe arg gln phe val glu ala cys gly gln ala leu ala val asn glu

3842 xxxxxxxx Coiled coil 2 xxxxxxxxxxxx 3872 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
CGT CTG ATT AAA GAA GAC CAG CTC GAG TAT CAG GAA GAA ATG AAA GCC AAC TAC AGG GAA
arg leu ile lys glu asp gln leu glu tyr gln glu glu met lys ala asn tyr arg glu

3902 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx 3932 xxx|

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FIG. 6A (cont.)

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ATG GCG AAG GAG CTT TCT GAA ATC ATG CAT GAG CAG ATC TGC CCC CTG GAG GAG AAG ACG
met ala lys glu leu ser glu ile met his glu gln ile cys pro leu glu glu lys thr

3962 3992
AGC GTC TTA CCG AAT TCC CTT CAC ATC TTC AAC GCC ATC AGT GGG ACT CCA ACA AGC ACA
ser val leu pro asn ser leu his ile phe asn ala ile ser gly thr pro thr ser thr

4022 |xxxxx PBM xxxxxx|
ATG GTT CAC GGG ATG ACC AGC TCG TCT TCG GTC GTG TGA TTA CAT CTC ATG GCC CGT GTG
met val his gly met thr ser ser ser val val STP

4082 4112
TGG GGA CTT GCT TTG TCA TTT GCA AAC TCA GGA TGC TTT CCA AAG CCA ATC ACT GGG GAG

4142 4172
ACC GAG CAC AGG GAG GAC CAA GGG GAA GGG GAG AGA AAG GAA ATA AAG AAC AAC GTT ATT

4202 4232
TCT TAA CAG ACT TTC TAT AGG AGT TGT AAG AAG GTG CAC ATA TTT TTT TAA ATC TCA CTG

4262 4292
GCA ATA TTC AAA GTT TTC ATT GTG TCT TAA CAA AGG TGT GGT AGA CAC TCT TGA GCT GGA

4322 4352
CTT AGA TTT TAT TCT TCC TTG CAG AGT AGT GTT AGA ATA GAT GGC CTA CAG AAA AAA AAG

4382 4412
GTT CTG GGA TCT ACA TGG CAG GGA GGG CTG CAC TGA CAT TGA TGC CTG GGG GAC CTT TTG

4442 ref 13.1 4472
CCT CGA CTC GTG CCG GAA ATC TGA TCG TAA TCA GGG TAC AGA ACT TAC TAG TTT TGT CTA

4502 4532
GGA GTA TGT TGT ATG ACT AGG ATT TGT GCT ATT ATC TCA TTC AAC AAC ATA GAG CAA GAA

4562 4592
TAG TGA GCT AAC TGA GCT AGA CAC TCA ATT AAT CCG CTA CTG GCT TCA AGT CAG AAC TTT

4622 4652 ref 14.1
GTC ATT AAT CAT CGA CTC CGG GAC GGT CAT ATA TGT ATT ACA TTT CTA CAT TTT TAA TAC

4682 4712
TCA CAT GGG CTT ATG CAT TAA GTT TAA TTG TGA TAA ATT TGT GCT GGT CCA GTA TAT GCA

4742 4772
ATA CAC TTT AAT GGT TTA TTC TTG TCA TAA AAA TGT GCA ATA TGG AGA TGT ATA CAA GTC

4802
TTT ACT

FIG. 6A (cont.)

BAC sequences of Human CLASP 2

Ref 1.1

Sequence of BAC4 using primer HC2AS2, which spans nucleotides 327-346 of the cDNA. Exon sequence is underlined and represents nucleotides 356-375.

TTTCTACAGNGTNTACTCAGGTATGTGCTCCTTCAACAAAATTAGCAGTTGCTGCTCT
 GTGACAAAGTTTGCACCATTTTGAAGAAGAAAAAATCCTAATGTGTTATATTACTA
 TATTTTACTCTATAGATCTTTTTCTAAAGAAAGAAAGTACAAGTGAAGTGCTTATAT
 GTATTCATATAAATGACTAGTACAAGCATCATTTTGAACAGATTTCCCCTTTCATTG
 GAGGATCTTCTTGATGTTATTTGTACACGATCAATTTTGTAGTCTTAATAAGATGAGGC
 TGGGTGTGGTGGCTCACACCTGTAATCCTAGCATTTTGGAGGCCAAGGTGGGCAGAT
 CACTTTAGCCCAGGGGTTTGAGACCAGCCTGGCCAACATGGCAAAACCTTGTCTCTA
 CAAAAATACNAAAATTATCCAGGCATGGTGATGTGTGCCTGTAGTCCCAACTNCCTAG
 GAGGCTAGGGGTAGGGGGATTGCAAGAGGCTGGGAGGGTCAAAGCCCNAANTGAG
 CCATTGGTNCATGTCACTTGGACCCCAAGCNGGGGNGANCAAGAGCAAAGGACTNN
 TGTNNTTTANAAAAAAAACCGGGCTACCATAACNNACCAACCCNCNNACCTACCCNACC
 TTTCCANNTTAAAAANAAGGCTTTGNCTTGCANAGGAAAAANCAAAATNNCC

Ref 1.2

Sequence of BAC26 using primer HC2AS2, which spans nucleotides 327-346 of the cDNA. Exon sequence is underlined and represents nucleotides 351-375.

TCTGGTTTCTACAGTGTATACTNAGGTATGTGCTCCTTNAACAAAATTAGCAGTTGCT
 GCTCTGTGACAAAGTTTGCACCATTTTGAAGAAGAAAAAATCCTAATGTGTTATAT
 TACTATATTTTTACTCTATAGATCTTTTTCTAAAGAAAGAAAGTACAAGTGAAGTGCTT
 ATATGTATTCATATAAATGACTAGTACAAGCATCATTTTGAACAGATTTCCCCTTTC
 ATTGGAGGATCTTCTTGATGTTATTTGTACACGATCAATTTTGTAGTCTTAATAAGATG
 AGGCTGGGTGTGGTGGCTCACACCTGTAATCCTAGCATTTTGGAGGCCAAGGTGGGC
 AGATCACTTTAGCCCAGGGGTTTGAGACCAGCCTGGCCAACATGGCAAAACCTTGTCT
 TCTACAAAAATACAAAAATTATCCAGGCATGGTGATGTGTGCCTGTAGTCCCAGCTAC
 CTAGGAGGCTAGGGTAGGGGGATTGCAAGAGGCTNGGAGGTCAAGGCCCGAGTGA
 GCCATGGTCATGTCACTGCACCCCAAGCCAGGGCCGACAGGAGCAAGACTNTTGTNT
 CAAAAAAAACAGNAACCAACANCCAACAACAACACNACCTTTCNGCAAAAANAAGC
 TTGCTNCAANGAAACCAAAATGNCTTCTTNTTTTCCCCCN

Ref 1.3

Sequence of BAC26 using primer HC2AS2, which spans nucleotides 327-346 of the cDNA. Exon sequence is not found within this sequence. This sequence most likely represent intron sequence since this sequence matches the intron sequence found in the previous two BAC sequences.

AGNNNNNCCCNCTACNCCACTTTTAACCTTTTGAAAAACACAGTGTNTNCTCAANTATG
 CGCTCCTTCACATATTAGCAGTTGCTCTGTGACATAGTTGCACCATTNTGCAAGA
 AGAAAAATCCTAAGTGTNATATCACTATATNNNTACTCTATAGATCTTNTCTAAAGA
 AAGAAAGTCAACTGATGTGCTTATATGTATNCATATAAATGACTAGTACATGCATCAT
 TTTGCAACAGATNTCTCCTCACATTGGAGGATCTTCTNGANGNATTCGACACGATNAN
 TATTAGTCTNAATAAGATGANGCTGGTGTGGNGGTACACTGNATCTAGCATNTGGAN
 GCATGTGGCAGACACTTANCCNCGGTNGAGACAGCTGTCACTGNCNAACTGTCTCTN
 TAAANCAAANNCTCCGCNGGNGATGGGCTGAGCCAGTCCTAGNNGCTAGNTAGNGAT

FIG. 6A (cont.)

GNNGAGNTGTNGCACGNCGAGNGAGCATGNTCTGTACTGACTCATCAGGCGNCNACA
 CGNTCTGTTCNAAAACATACCACACACACTCNCACCTNCGCAAAATTGCTCTNNAAAN
 ATGCTTNTTTCACACNGNTNCAATCNCTATATNNTCTTCTATTCTNCNACGTNTNATTA
 NNATCTTNCNCTGCANAAACNATNCGNCCACCTNNANNACCTTANGCTTNGTTTCACGC
 TTATAGCTCCCCCTACACNTNNCAGCNNTTNCNNGTGAAGGGCCNCCCGAATCTACGA
 NCATACTCTCTCCGTATATNGCCTCGGTCANCGCCATCTGCTGTNTNCTCNCNTNG
 CNNTTNANCNGTNCGCTATCTCTNNNCCGGATCCNCCATATNNTNNTCTACTTAN
 AGCGTAANNTNTNCNCNCACTANTCACAACCTTNTNCTNNAACTCTATCTNCTCCTCT
 CTACCACCTCACTTACTACCTNTTCAACNANTCTCCTTCNCTNTCCACTGATCTCCACA
 TAGCTGCTNTACTCGCCANTTTATCATATNCACACNCTCTACGCTNNNTNT

Ref 2.1

Sequence of BAC4 using primer HC2S1, which spans nucleotides 1107-1126 of the cDNA. Exon sequence is underlined and represents nucleotides 1079-1097.

CTTGATTNAAAGAGGGTCTGCAGGAAGAAGTGTGTAGTCATAAATACCTCACTGGA
 TATTTTATACAGGATTCTAAAAACCTATTAGCAATAGTATGCTAGAAATAGTCATTA
 GCTTCTTGACCTTCTTAGAACTGCACACTCTATTGCACTGTACAGATTTCAGGATGGC
 TGCAGGGATTGATTTGAAAACTAAGGACACATTTCAATAAACAATGTCTTCAATTGAT
 TTTTAGGGCTCCTCCTACTTCAATGAAGGACTTCAGGTAGCTTATAATTACAGACACA
 GGCTCAATAACAATAAAAAAATTAGTAAGGCAGAGCTTTAAAAAAGGAAAAA
 GATAATTCTACCAGAGAAAGGCTACATGGTGACTTCTGTTACCAGTAACAACCCCG
 CACTACCTTTGGGTCTCCAGGAGCAAAACAGCTAATGTAGTTGTTGATCTGCTTGAAG
 ACAAGCCCCTGTCCATGAAGGTGAAACATCTCTGTGGAGGAAAACAAGCAAAAAAG
 TTATTTCAAGGTCCAAACATTTTCGGAAATTTGGATTCAAAGCAGGCATTTATTGCTAAT
 AAGTTTATCCACTGACATAAAAAACATGCCTTCAACATTGCCAGAGCACCTACTCTAT
 TNTAGTCNCN

Ref 3.1

Sequence of BAC4 using primer C96AS, which spans nucleotides 1443-1452 of the cDNA. Exon sequence is underlined and represents nucleotides 1370-1422.

AATCAGCAGACCAAACAGAGGCAGGTAGAGGGTGGCTATCCTTGCCTGATGGCTCTG
 AAAAGAAGACACACATGGTAAGTTTGACCCAGGATTCTGAGAACCGAACATAAGTTGG
 TGCTGACCATCTCCTTTATTTGGATCCTTCCTATAAAGACAGATATTTGATTTTAGTCC
 CAAAATAGAGCAAAATCTTAGTGCTGTTACCATGAATTTTCTAACTGATTACTTTCTTT
 ACACCACTTAAAATAAAGGACATTATCAATGCACATTCCTTCCATTGGGGACCACTCA
 CCCTTGAAGCATATCTGTTCATCAAAAGAATGCTTTATCAGCAGGTTCTTGAGCACACT
 GATGGCGATCAGACGGACCTCCCGGAACCTCCTGGAGGGCTGTCCCCACCTCCCTNAG
 TAACAGTCCCACCAAGAAGTGGTTTCTGCAGAACTCATCTGTTAATGAGTAGTCAAGC
 TGGGAGGTCTGAAATGAGGATAGAACTACTTTGNGTTAGGAAAGATGCAATGCTCT
 TTTGAATAAAACAAACAAACCAAAACNAACAAAAAAGATGCAATGCTCT
 ATTTCAAGCCCACCCTGGGGTNGGTCAAAGAGATGATCAGNANTTTGGCNTTNAAT
 GAAGAAAGAAATNAATTNTCCAGGGGNTGTTCTNCTTTTAGCACANGGAGGGATNT
 TAANTGAAAACCAATTTAAATCCAATTNAGGNG

FIG. 6A (cont.)

Ref 4.1

Sequence of BAC4 using primer C2AS5, which spans nucleotides 1716-1735 of the cDNA. Exon sequence is underlined and represents nucleotides 1602-1703.

TTCCTTTCTGCAAGGCTGTTCCCGAATCTGTGCTTATGAGAGATCCTCTCGAATCAGC
ATTTCTCACACTGTTGATGTTTGGAGTTGAGGTTGTATATGGAGAAGCTAAATGGAAA
 TCAAGCCAACAATAAAGTTTTATTAAGACAGAACAAAATAAAGATGAGTACTGAACTT
 TAAGGGAAATTGCTTTTATTGCACTTATTTTTTCTGTTAGGAAGTTGGCTCAAGAGTT
 GCATTCCATTACTTCACCTTTAAAGAACCAGGTCATATACAATGAGATAAAAAAGAAAC
 TAGTCTGAAACATTGAGATGTAAACATCAATTCACCTGTTAGAAACCACCTTTGATCG
 CTAAAGACTAAATGCATACCTGTTTCAGAATGTGATAGAATGAAGACTTAAAAAAATT
 AAAAGATAAAATCCACCTACAACATCAAAATCACAAAATTAAACCACACAACAACTTG
 TAGCATTCAAACCTGGTAATAAAACACTGAGGAGCCTACCCAACTCTGAGGGGTGTCAT
 GGGGTATTTTAAATTTTCGAGGAGAACACAGTGATATGTGACCTCAGCCAGAAGCTG
 CTGTTTNAGCAGCAGGTTGGTGCTATGCTCCTTTTTGAAGACATATTTGTGAAGCTGG
 GTATTTTGGGGGGCCTGCTTATGATAAAAANGGCAAGGTNTTCAATGNAGGGGN

Ref 4.2

Sequence of BAC26 using primer C2AS5, which spans nucleotides 1716-1735 of the cDNA. Exon sequence is underlined and represents nucleotides 1602-1703.

TTCCTTTCTGGAAGGCTGTTACCCGAATCTGTGCTTATGAGAGATCCTCTCGAATCAG
CATTTCTCACACTGTTGATGTTTGGAGTTGAGGTTGTATATGGAGAAGCTAAATGGAA
 ATCAAGCCAACAATAAAGTTTTATTAAGACAGAACAAAATAAAGATGAGTACTGAACT
 TTAAGGGAAATTGCTTTTATTGCACTTATTTTTTCTGTTAGGAAGTTGGCTCAAGAGT
 TGCATTCCATTACTTCACCTTTAAAGAACCAGGTCATATACAATGAGATAAAAAAGAA
 CTAGTCTGAAACATTGAGATGTAAACATCAATTCACCTGTTAGAAACCACCTTTGATC
 GCTAAAGACTAAATGCATACCTGTTTCAGAATGTGATAGAATGAAGACTTAAAAAAAT
 TAAAAGATAAAATCCACCTACAACATCAAAATCACAAAATTAAACCNCACAACAACTT
 GTAGCATTCAAACCTGGTAATAAAACACTGAGGAGCCTACCCAACTTTGAGGGGTGTC
 AATGGGGTNTTTTTAAATTTTTCGNGGGANANCCAGTGNTATGGTGACCTTCACCCA
 AGAAGCTTGTTTGTGTTNACCAAGCNAGGTTGNCTNTGCTCCTTTTTAGAAANACNNTA
 TTTTNNNAAATNCTGGNTTTTTTNNNGNGGCCCCCTNCNTTNT

Ref 5.1

Sequence of BAC4 using primer C2S6, which spans nucleotides 1686-1705 of the cDNA. Exon sequence is underlined and represents nucleotides 1724-1736.

TTCCTGGATAAGGTAATTGCTTTTACCCAACACAAATGTTTCTTATAATCAATGGATT
TAGCCCAAAGTAAACGTAATTCATGTTCTAGTGCTTTTAAAGTGTGACCTTTTGTTTT
TTTCTAAACCACCCGGCTGACCTGGAGTAGGTGATGAGAGCTTTAAGGTTGGGGCCC
ATTCCTTGAAGTGCTCTGATTCTGTTTCCAGTACCTCAGATCCTGGGCAGGGTTTGC
AGTGGAGCGTCTTGAGTGAATGGCTCTGGTGGGTTGAACGGGGAGGGACTCAAAAT
GCTGCCCATCTCAATTTCTGTAGTCTTTTTATTTATTTATTTATTTTGGACAGAG
TCTCGCTCTGTGCCCCAGGCTGGAGTACAGCGGCACGATCTCAATTNACTGCAACCT
CCGCCTCC: TGGGTTCAAACGACTCCTCTGCCTCAGCCTCCCCAGCAGC: TGGGACCA
CAGGCACAAGCCACCACCGCCCGGCTAATTTTTGTNTTTTAGTA: GAGAT: GGGGTT
TCACCATATTTGGCCAGGCTGGGCTCAAACCTCTGACC: TCGTCATCCGCNCCCTCGG
NCTNCCAAAGTGCTTGGGATTNCAGGCNGTGAGCCCACTTACACCTNGGGCAATTCC
CTGTNAGTCTTTTTTACCAGAGACACCATCATTCAACACAGCTTTTCCACCCACAA

FIG. 6A (cont.)

Ref 5.2

Sequence of BAC26 using primer C2S6, which spans nucleotides 1686-1705 of the cDNA. Exon sequence is underlined and represents nucleotides 1712-1736.

TGAGAAGAGCAATTTCTGGATAAGGTAATTGCTTTTACCCAACACAAATGTTTCTTA
 TAATCAATGGATTTAGCCCAAAGTAAACGTACTTCATGTTCTAGTGCCTTTTAAGTGT
 GACCTTTTGTTTTTTTCTAAACCACCCGGCTGACCTGGAGTAGGTGATGAGAGCTTTA
 AGGTTGGGGCCCATTCCTTGAAGTGCTCTGATTCCTGTTTCCAGTACCTCAGATCCTG
 GGCAGGGTTTGCAGTGGAGCGTCTTGAGTGAATGGCTCTGGTGGGTTGAACGGGGA
 GGGACTCAAAATGCTGCCCATCTCAATTTCTGTAGTCTTTTTATTATTTATTTATTT
 TTTGAGACAGAGTCTCGCTCTGTGCGCCAGGCTGGAGTACAGCGGCACGATCTCAAT
 TCACTGCAACCTCCGNCCTCCCTGGGTTCAAACGACTCCTCTGNCTNAGNCTCCC:AGC
 AGCCTGGGAACACAGGCTCANGCCACCACGCCCGGCTAATTNTTGAATTTTNAGT
 AANAAATTGGGGGTTCTCACCATNTTGGCCCAAGNCTTGGGCCTAAAAACCTTNCTNA
 CCNTCGNCATTNCNCCCCNACCNTGGGCNCTNCTCAAANGNGCTTGGGGATTANC
 ANNCGCNTTAACCCCCNTATCACCGTGGNCCTTAATT

Ref 6.1

Sequence of BAC4 using primer C2S7, which spans nucleotides 1918-1937 of the cDNA. Exon sequence is not found within this sequence. Since the primer is directed against exon sequence we presume that sequence derived from C2S7 is intron sequence.

NAGNGNGGGTTTNAGNCGTTTGAAGCCTGNNACGNGGTGNGTGCTNGAACTCTGTGG
 GCTTTCAGGTACTGGGGTATCTGGGAGCCTGCTGTTTGCATTGCTAGTGCATCAGAC
 CAGGGCTTTTCTCCCTGTAGCTGCTACTTATACACATAGCTCTAACTGAGATGATT
 CTCCAGACAACTGATGCAGAGCAGCAAAAGCTTCTGCCGTTCTCCCTTCTAGGAGT
 GTCTCCTTTCTTTGGAAAGAGATCATGAGGGGCTAGATTGTAATGAAGTGAGGCTCA
 GTGCTTGAGCACATCCGGTAAAAGTTCCAATATATTGGTCATAAAGTTTCTCATTCTT
 TATAGCAGTTAATTTCTCTGGCTCATGAGTTTTCTTAGTTTTAATCTGACTTTTAAATT
 AATGTCTCCAGCACCAGTCATATCCCCAGGGCAAACCTCAAAGGCATGAGAGGCCAGA
 CTCGGGTCTTGGTCATAGCAACCCCTGTCTAGGGCCTTGGTCCCTGCCTCCGCTTGT
 GTGCTGTGGCGCAGGTCCTATGGGCCCTTAGGAAACAGGACCACCCTGTCGCACCCC
 CTACAGAGACCAGCCAAGTTTGACATTAGATCACCGTAGCAATGTNTGCAAATTCCA
 GTTCTTGCTAAAACAGGTTAAGCCTTGCAGCCACTTTATCTGTAAGTGGCNGAGGTT
 TTGACATAAAA

Ref 7.1

Sequence of BAC4 using primer C2S8, which spans nucleotides 2143-2162 of the cDNA. Exon sequence is underlined and represents nucleotides 2182-2219.

CTCTCGACACGCTGTTTCTATTAACATTGGCGTTTAAGGTTTGTATCAATTTGCTGTT
 CGNGGTTCTAGTTTTACCTTTCACATTCATTCTGCTTGGTAAGCTCAGTGAGCACAAA
 CTTACTATGTTGCATTTTTACTTCAGCAATTATTTTTGTCCCTGTAAGGAAACCATTAA
 TCTTTAAATTCCTTTAATGAAATCATTCCACAGTGAATGGCTTGAATGCCCTGAAATA
 AAATTTAACTGGTCAGTGTGTGCTGCGCGCTTGGGTATGGTGGAACACGGTCTCTG
 GAGGCAGTTAACTCTTGGCTCGAACCTTGAGGATGGTGAATATAGGCACCTAATCAG

FIG. 6A (cont.)

GCATTTCTGCCTTGAATATCTTTAAATATATCCAAATGTTATAGCGTTTAATTAGATT
 TTATGTAGAAAGGAGCAATAAACACAAGACACATGTTTTTCAGTTTTTTATCTGTTACT
 GCATTAAATGATAAAAACGTTTTGGAGATAGAAAATGAAAGGGGTTTTTTTTGTCT
 TGTTTTAAAGTTTTAGCAAATAATATTCAAGTAGGTGGAGATGGACTCTTCACCACTC
 TCCTGTTTTTAGGAACCAATACTTTTTTCATTCTTGCTAAATGATTACTTCCATTCTA
 GCATAGAAAAGGAGAAAATTGGAATGAGTGTATAT

Ref 8.1

Sequence of BAC4 using primer C2S9, which spans nucleotides 2992-3011 of the cDNA. Exon sequence is not found within this sequence. Since the primer is directed against exon sequence we presume that sequence derived from C2S9 is intron sequence

CGCTTTNAAATNCCAGCCGCTACTGCGGGGCGNTNAATTTCGAAACGTGTTGTTNTCT
 GTGATGCCTGGCTCTGATTGTGTGGGATTGGTCATCAGTGGCGGTTGGCAGNTGGGG
 TTCATGGAAGCGGCCATGGGGACTGATGGCAGGCCCTTGGATTGCCACCGCAGAGCC
 TGGCAGTGTCTTTGGTCTGCATTCCCTACCGGCGAAGTCTCATTTACCTCACGTGTTA
 TCTCTTGGAAGCATTCCCTTAGCGGGCTGTGTCTACCCTTCCATCCTCTCGTCCAAA
 CTCCCCCTCCTTCTCTGTCTGTCTCCTTCCCATCCTCTTCTCCCCAGTTCTTCTCCT
 ATGTTCCCTCCTCAGTGGTCTTCTCTTCCCTCTGTTTGACTTTCCAAGGTCATTTTGACTG
 TTCCTGTCTCCAACTACAAAGATACTAAAATCTCACCTAACCCTCTTCTTCTTTCTTA
 ATGAAAGAATGTTTTTCAGTCCATCCCAAATTTGTGTGGACTTCACAAACCTTCTCTAA
 AATGGAGCCTTTTCTCTTCCCTACTCTTGACTAGNTGGTAAACGCTCCATGTTCTTGGC
 CAGAACTCCCTGGTGAGTAGCGTCACTCCCACTTTCTGTGCAGAACCAAGCCTCCT
 AGAAAACCTCTTGCANCTGAGTGGGTTGGGACACGCCCTTTNTTTGGG

Ref 9.1

Sequence of BAC4 using primer C2AS10, which spans nucleotides 3276-3295 of the cDNA. Exon sequence is underlined and represents nucleotides 3147-3234.

TTTANACCNATNTATCCGNGTCAGTTANAGGAGTCTCTGAGAAATTTCCGACAGCGGT
GTGAGTTTGGGTTCCTTGTAATATACTCCTTTCCATCTTCATCTTCAAAGAATCCCT
 GTGACATAAAGCACAATTAGAGCTATCCCTGAACGTAAGCCCAGGGCTTACCACCTA
 GGAAGCGTTCTTTTATTACAAGGGGGGAAAAAAGGAATGGGTCTAAAAATCCAGCTG
 AAATGGGCTTTCTGAATGAGAAAGAAAATGCTAATAACATGAAGTCTAGGTGCAAAG
 GTAAAGGAAAAACACAACATTGCAAACCTTATTCAAGAATGCAGTCATTAAGTGTTGAG
 TGAAATGAAAGATTTTGGATACAAGACTAAGCTGTCCCAGGGAAGTCTAATGGGAGT
 CAAGCCTGTTTCACTTTCCCAAGAAGCAGAACTCACTANAAAATGATGAGCAGCCCA
 CGACAGGCAGGCTCAGAAGTGGACATGCCTCCCTTCTCCTGATGGCTNCCATGCACA
 CAGGATTTTATGGCATGAACTGAAGCGTTTGGGGGTCTGGAGTAAGTTTAGTAAAAG
 TTAGGTAAAGCTTGTATAAATTGTATTTTGTCTTACCCGATGAGAAAAAAAATATTN
 AAGACCTGGTAGCTTCAATATTCAAGAAAAATATTTTTCATNTCACCCG

FIG. 6A (cont.)

Ref 10.1

Sequence of BAC4 using primer C2S11, which spans nucleotides 3167-3186 of the cDNA. Exon sequence is underlined and represents nucleotides 3231-3296.

NGNANGTGGAGCCNCGANCCAGGGACAATCTNAACCTNCTTAAACTGTACTCGGATN
AATTTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGCAAGGTATTGACCATGTT
 TGGANAAGTTTCATAGCAATGTAATGTTGTGATNCGATTACATATNATATATTTTAA
 ATGTNTATAGAAAAAACACANGAAAAATATTAAGGATTGTTGGCCCGTGAGTGGCA
 GGTGTATNTTCTTNCTGATCCTTTAGNGCCTTCCATTACATGCNTGACATTAAAAAA
 NCTTTATCGCCTAATTTTTGAAACATCTAATTTTACAAAATAATTAACCGTNTGGCCAN
 GNATATTNTCATTTTTAGGNCCAGCTATTTAGAAACTCTGACANAAATGAGGGGCTGT
 GGCTTNCCTNCCCTNNACTTGNCCCTCTTTCNNGNATGTACCACATGAACTTGNCNCCT
 CTTTCNNCTNACCGGGTGGCATGTTANAGGACAGGTTGAAACCNCANTNGGGCNGGA
 NTTNGGTNNAATTGGGACACAATGGTACNANGCTCTATNGGAATNGAACTCTCCCN
 ACNNCNGTGNCCNTGGGGAAAAATGNGNCNNATTCATTTTN

Ref 11.1

Sequence of BAC4 using primer C2S12, which spans nucleotides 3474-3493 of the cDNA. Exon sequence is not found within this sequence. Since the primer is directed against exon sequence we presume that sequence derived from C2S9 is intron sequence

AGNANNGTNNNGCAGCTGCANNTCTGGACCCANAGGCCGCANGGGCACGAGCCNNG
 ACACGCTCGGCAAAGAGCTGTCCAGAGGGATTGAGAAGCTTCAGGACTGGAAGGGTC
 TTTCGAGCTCAGTTAGCCACCCCCACACCCATTTAGTTTCACATTTATCTAGTGCTT
 CCTTTTGAATACTTGGGATGTTTTTCTGTTGATCTGTTGGCACTTCCTTCTCCACAA
 GACCAGAAGCTCATATCCAATCTAAGGTCACTTACCCTTCTGAGAATCTGATGAAAT
 GGCGTGCTTATGTGCCTAGATGCTTTTGCACACAGTCTAAGGTGACTTATGGACTCC
 AGGTCCAGCAGCCACACCCAGTCCTGGGTCTCCGCACAGGGAGGGACCCGTCTTCAC
 ACACCTGTCTCAGGTTCTAGCATTGGGCTGCTTCAGCGGTCTCAGGCTGTGAGTAA
 TGGGATGTGAGCTTGGATCGCCCCACGCTGTTGNCCCCCGGGGGGCTTGGCCAGCTG
 GCCACTNGAAATGCCTCCTTTTGCCAGGAAAGCTCACTGCATTTCAATGGGGNTTN
 TCCACGAAGTTCANCTTTANGGG

Ref 12.1

Sequence of BAC4 using primer C2S13, which spans nucleotides 3645-3664 of the cDNA. Exon sequence is underlined and represents nucleotides 3683-3699.

AGNAAGGTNNCTCANTNAANNCAGCGTGAGNGTTCAGGTGAGCCAGGCACAGCAGGC
 CGGAGGGGCAGCAGGGGACGTCCCTTGCCCCTGGGTGACTTGAGAGTCGTTTCCACTAA
 CAAGGTCTACTTGAGAGCCTCGGTTTACCAAGTGATCCCTGCTCCCTTCCCCCAACGT
 NTGTGACATTTCTCCTGATATCAGAGGGGGAGGAAACCTCATGATCCCTGCCCCCG
 CCCCATGAGGACTGACTGTGGGGACAAAGAGCCAGATCTCATAGACTACCCTGATTT
 GTCAGTATTTGGGGAATTCTGGGTGCCTGATTAGAAGCATCAAGACTCTTCTAAATNC
 AAAGAAGTGTGGAGAGCAGTAGATTTTCTATAAAACTGGTGTGTGCTGGTTTCTATGA
 AAATTGGATCCAAAAAAGTCCTTAAGTTTACCCTCTTAATGGNATCTTTTGATTAAT
 GGAATTCATTATTTTAATATAGCCCAATCAATCCAATTTTCTTTATTGGTAGCATTTT
 TATGTTCTCTTTAAAAAATCTTGGNCTACCTCCAAAATTTACAGATGTTCTCCTAG
 GGTTTCTCCTTTTGGTTCAAGCATCCATTCAANGTCTTGCAGTCCATTCTGGGG

FIG. 6A (cont.)

Ref 13.1

Sequence of BAC4 using primer C2S14, which spans nucleotides 4289-4308 of the cDNA. Exon sequence is underlined and represents nucleotides 4321-4448.

GACTTANATTTATTCTTCCTTGCAAGTAGTGTTAGAATAGATGGCCTACAGAAAAAA
AAGGTTCTGGGATCTACATGGCAGGGAGGGCTGCACTGACATTGATGCCTGGGGGAC
CTTTGCGCTCGAGGCTGAGCTGGAAAATCTTGAAAATATTTTTTTTTTTCCTGTGGCAC
 ATTCAGGTTGAATACAAGAACTATTTTTGTGACTATGTTTTTGATGACCTAAGGGAAC
 TGACCATTGTAATTTTTGTACCANTGAACCANGAGATTAAAGTGCTTTTATATTCATTT
 CCTTGCAATTAAGAAAAATATGAAAGCTTAAGGAATTATGTGAGCTTAAACTAGTCAA
 GCANTTTAGAACCAAAGGCCTATNTTNATAACCGCAACTATGCTNAAAAGNACAAAGT
 AGTACAGNATATTGNTATGTACATATCATTTGGTAATACACNCCNGGCNTTCTGTACA
 TATATGTATTACATTTCTACNTTTTAATACTCCCNTGGGCTTATGCCNTTAAGGTTAA
 NTTGNGATAAATTTNGGCTGTTCCNGTNTATNCNATACNCTTTT

Ref 14.1

Sequence of BAC4 using primer C2AS15, which spans nucleotides 4680-4700 of the cDNA. Exon sequence is underlined and represents nucleotides 4660-4683.

ATGAGAATGTAATACATATATGTACAGAATGCCAGGACTGTATTAACAATGATATGTA
 CATAACAATATACTGTACTACTTTGTACTTTTCAGCATAGTTGCGGTTATTAATATAG
 GCCTTTGGTTCTAAACTGCTTGACTAGTTTTAAGCTCACATAATTCCTTAAGCTTTTCAT
 ATTTTCTTAAATGCAAGGAAATGAATATAAAAGCACTAAATCTCCTGGTTCAGTGGTA
 CAAAAATTACAATGGTCAGTTCCTTAGGTCATCAAAAAGTACACAAAAATAGTTC
 TTGTATTCAACCTGAATGTGCCACAGGAAAAAAAAAATATTTTCAAGATTTTCCAGCT
 CAGCCTCGAGGCAAAAGGCCCCAGGCATCAATGTCAGNGCAGCCCTCCTGCCATGT
 AGATCCCAGAACCTTTTTTTTTCTGTAGGCCATCTATTCTAACACTACTCTGCAGGGAG
 AATAAAATCTAAAGNCCAGCTCAAGAGTGCTACCACACCTTTGTTAAGACACAATGAA
 AACTTTGGATATTGGCAGGNGAGATTTAAAAAAAATGTGCCCTTTCTTACCACTCCT
 ATAGNAAAGTCTGGTTAAGAAATAACCGTTGGTCTTTATTTTCTTTTNTTTCCCTTC
 CCTTGGGNCTTCCTGGGGCTCGG

FIG. 6A (cont.)

HC2A	-----
KIAA	ASGNLDKNARFS AIYRQDSNKLSNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----
KIAA	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLYDSQ
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----VLHHHQNP EFYDEIK
KIAA	KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTSAFAAVLHHHQNP EFYDEIK
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	IELPTQLHEKHHL L L T F F H V S C D N S S K G S T K K R D V V E T Q V G Y S W L P L L K D G R V V T S E Q H I
KIAA	IELPTQLHEKHHL L L T F F H V S C D N S S K G S T K K R D V V E T Q V G Y S W L P L L K D G R V V T S E Q H I
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	PVSANLPSGYLG Y Q E L G M G R H Y G P E I K W V D G G K P L L K I S T H L V S T V Y T Q D Q H L H N F F Q Y C
KIAA	PVSANLPSGYLG Y Q E L G M G R H Y G P E I K W V D G G K P L L K I S T H L V S T V Y T Q D Q H L H N F F Q Y C
rat	-----
HC4	-----
HC1	-----
HC3	-----GPGPARSTV S I S L I S N S A R V
HC5	-----
HC2A	QKTESGAQALGNELVKYLKSLHAMEGHV M I A F L P T I L N Q L F R V L T - R A T Q E E V A V N V T R V
KIAA	QKTESGAQALGNELVKYLKSLHAMEGHV M I A F L P T I L N Q L F R V L T - R A T Q E E V A V N V T R V
rat	-----
HC4	-----M E I Q V L I R F L S V I L M Q L F W V L P N M I H E D D V P I S C P M V
HC1	-----M S F L P I I L N Q L F K V L V - Q N E E D E I T T T V T R V
HC3	NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAES
HC5	-----

FIG. 6B

HC2A	IIHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSTN	
KIAA	IIHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSTN	
rat	-----	
HC4	LEHIVSKCHEEGLDLSYLSSFIKYSFRPGKPSAPOAPLIHETLATMMIALLKQSADFLAIN	
HC1	LPDIVAKCHEEQLDHSVQSYIKFVFKTR---ACKERPVEDLAKNVTGLLK-SNDSPTVK	
HC3	TQAMDRSCNRMSSHTETSSFLQTLTGRLP---TKKLFHEELALQWVVCSG--SVR---E	
HC5	-----	
	Cadherin Cleavage	
HC2A	KLLRYSWFFFDVLIKSMAQHLENSKVKLIRNORFPASYHHAAETVVMMLMPHITQKFGD	
KIAA	KLLKYSWFFFDVLIKSMAQHLENSKVKLIRNORFPASYHHAAETVVMMLMPHITQKFRD	
rat	-----	
HC4	KLLKYSWFFFEIIAKSMATYLLEENKIKLTHGQRFPPKAYHHALHSLFLAIT-IVESQYAE	6.1
HC1	HVLKHSWFFFAIILKSMAQHLEIDTNKIQLRPPQRFPEYQNELDNLMVLSHVIVWKYKD	1.2/1.2/2.1/2
HC3	SALQQAWFFFEILMYKSMVHHLYFNDKLEAPRKSRFFPERFMDIDIAALVSTIASDIVSRFQK	
HC5	-----	
HC2A	NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL	2.1
KIAA	NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL	
rat	-----	
HC4	IPKESRNVNYSLASFLKCCLTMDRGFVFNLIN---DYIS--GFSPKDPKVLAEYKFEFL	7.1
HC1	ALEETRRATHSVARFLKRCFTFMDRGCVFKMVN---NYIS--MFSSGDLKTLQYKFDL	3.1/3.2
HC3	DTEMVERLNTSLAFFLNDLLSVMDRGFVFSLIKSCYKQVSSKLYSLPNPSVLVSLRLDFL	
HC5	-----	
HC2A	RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL----DYSLTDEF	
KIAA	RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL----DYSLTDEF	
rat	-----	
HC4	QTICNHEHYIPLNLPM-----AFAKPKLQR-----VQDSNL----EYSLSDEY	
HC1	QEVQCQHEHFIPCLPIRSANIPDPLTPSES-----TQELHASDMPEYSVTNEF	4.1/4.2
HC3	RIICSHHYVTNLNLPCLLTPPASPSVSSATSSQSSGFSTNVQDQKIANMFELS--VPF	
HC5	-----MNADTAPTSPCPSIS---SQNSSSCSSFQDQKIASMFDRTSRVPA	
HC2A	CRNHFLVGLLLREVGTALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT	3.1
KIAA	CRNHFLVGLLLREVGTALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT	
rat	-----	
HC4	CKHHFLVGLLLRETSIALQDNYE----IRYTAISVIKNLLIKHAFDTRYQHKNQQAQIAQ	8.1
HC1	CRKHFLIGILLREVGFALQEDQD----VRHLALAVLKNLMAKHSFDDRYREPRKQAQIAS	
HC3	RQOHYLAGLVLTAVILDPAEGLFGLHKKVINMVHNLSSHDSDPRYSDPQIKARVAM	
HC5	SSTS-SPGLLFTLAAALDAEGEGISEVQRKAVSAIHSLLSSHDLDPRCVKPEVKVIAA	
HC2A	LYLPLFGLLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH	
KIAA	LYLPLFGLLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH	
rat	-----	
HC4	LYLPLFVGLLLIENIQRLAGRTLYSCAAMPNSASRDEFPCG-----FTSP--AN--RGSLS	9.1
HC1	LYMPYGMLLDNMPRIYLDKLYPFTVNTSNQSRDDLSTNGGFQSQTAKHANSVDTSFS	
HC3	LYLPLIGIIMETVPQLYDFTEHNRGRPICATDDYSE-----SG---SMIS	
HC5	LYLPLVGIILDALPQLCFTVADTRRYR---TSGSDEEQE-----GA---GAIT	
	4.1/4.2	
HC2A	KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNLSPERNSEKSNSLDKHQOSS	5.1/5.2
KIAA	KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNLSPERNSEKSNSLDKHQOSS	
rat	-----	
HC4	TDKDTAYGSFQNG-----HGKREDRSGSLIP-EGATGFPDQGNLTGEN-----TRQS	10.1
HC1	KDVLNSIAAFSS-----IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPL	3.1
HC3	QTVAMAIAGTSVPQ-----LTPRGSFLLTSTSGRQHT-----	2.1
HC5	QNALAIAGNNFN-----LKTSG-IVLSSLPYKQYN-----	

FIG. 6B (cont.)

HC2A	TLGNSVVRCDKLDQSEIKSLIMCFLYILKSMSDDALFTYWN-KASTSEIMDFFTTISEVCL	
KIAA	TLGNSVVRCDKLDQSEIKSLIMCFLYILKSMSDDALFTYWN-KASTSEIMDFFTTISEVCL	
rat	-----	
HC4	STRSSVSQYNRLDQYEIRSLIMCYLYIVKMISEDLLTYWN-KVSPQELINILILLEVCL	
HC1	ALIGSTLRFDRDLQAETRSLIMCFHIMKTISYETLIAYWQ-RAPSPEVSDFFSILDVCL	11.1/11.2
HC3	-----TFSAESSRSLICLLWVLKN-ADETVLQKWFDTLSVLQNLRLDLLLYLCV	
HC5	-----MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV	
HC2A	HQFQYMCKRYIARNQEGLG--PIVHDRKS-----QTLPVSRNRTGMM	6.1
KIAA	HQFQYMCKRYIAR-----TGM	
rat	-----	
HC4	FHFRYMCKRNRIARVHDAWLSKHFGIDRS-----QTMPALRNRSQVM	
HC1	QNFRLGKRNIIRKIAAAF--KFVQSTQNNGLTKGSNPSCQTSGLLAQWMHSTSRHEGKH	
HC3	SCFEYKGGKVFERMNSLTFFK--KSKDMRAK-----LEEAILGSIGARQEMV	
HC5	LCFEYKGGKQSSDKVSTQVLQ--KSRDVKAR-----LEEALLRGEARGEMV	
HC2A	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC	
KIAA	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC	
rat	-----	
HC4	QARLQHL-----SSLESS-----FTLNHSSTTTEADIFHQALLEGNTATEVS	
HC1	QHRSQTLPIIRGK---NALSNPKL---LQMLDNTMTSNEIDIVHHVDTEANIATEGC	12.1/12.2
HC3	RRSRGQLERSPSGSAFGSQENLWRKDMTHWRQNTKLDKSRAEIEHEALIDGNLATEAN	6.1/6.2
HC5	RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAELDQEALISCNLATEAH	
HC2A	LTALDTLSLFTLAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSIIY	7.1
KIAA	LTALDTLSLFTLAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSIIY	
rat	-----KLSRGHSPIMKKVFDVYLCFLQKHQSEMALKNVFTALRSIIY	
HC4	LTVLDTISFFTCQFKTHFLNNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS	
HC1	LTILDVLSLFTQTHQRQLQCCDCQNSLMKRGFDTYMLFFQVQNSATALKHVFASLRLFVC	13.1
HC3	LIILDLEIVVQTVS--VTES--KESILGGVLKVLHLSMACNQSAVYLQHCFAQALVS	
HC5	LIILDMQENIIQASS--ALDC--KDSLLGGVLRVLVNSLNCQSTTYLTHCFAQLRALIA	3.1
HC2A	KFPSTFYEGRADMCALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH	
KIAA	KFPSTFYEGRADMCALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH	
rat	KFPSTFYEGRADMCALCYEVLKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH	
HC4	KFPSAFFKGRVNMCAAFCYEVLKCCNSKLSSIRTEASALLYLFLMRNNFEYTKRKTFLRTH	
HC1	KFPSAFFQGPADLCGSFCYEVLKCCNHRSRSTQTEASALLYLFLMRKNFEFNKQKSIVRSH	
HC3	KFPPELLFEEETEQCADLCRLRLRHCCSSSIGTIRSHPSASLYLLMRQNFIGN--NFARVK	7.1/7.2
HC5	KFGDLLFEEVEEQCFDLCHQVLHHCSSSMDVTRSQCATLYLLMRFSFGATS--NFARVK	
HC2A	LQVVISVSQLIADVVGIGETRFFQQSLSIINNCCANSRDLIKHTSFSSDVKDLTKRIRTVLM	
KIAA	LQVVISVSQLIADVVGIGETRFFQQSLSIINNCCANSRDLIKHTSFSSDVKDLTKRIRTVLM	
rat	LQVVISLSQLIADVVGIGETRFFQQSLSIINNCCANSRDLIKHTSFSSDVKDLTKRIRTVLM	
HC4	LQIIIAVSQLIADVALSGGSRFQESLFIINNCCANSRDLIKHTSFSSDVKDLTKRIRTVLM	
HC1	LQLIKAVSQLIAD-AGIGGSRFQHSLAITNNFANGDKQMKNSNFPAPAEVKDLTKRIRTVLM	14.1/14.2/15
HC3	MQVPMSSLSLVGTSQNFNEEFLRRSLKLTILTYAEDLELRETTFPDQVQDLVFNLMILS	
HC5	MQVTMSLASLVGRAPDFNEEHLRRSLRILAYSEEDTAMQMTFPTQVEELLCNLNSILY	

FIG. 6B (cont.)

	Transmembrane	Ref.
HC2A	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKWTWLD SMARIHVKNGL LSEAAMCYVHV	
KIAA	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKWTWLD SMARIHVKNGL LSEAAMCYVHV	
rat	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKWTWLD SMARIHVKNGL LSEAAMCYVHV	
HC4	ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKWTWLD SMAKIHVKNGL FSEAAMCYVHV	16.1/16.2
HC1	ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLE SMAKIHARNGDL SEAAMCYIHI	
HC3	DTVKMKEHQEDPEMLIDL MYRIAKGYQTS PDLRLTWLQNMAGKHSERSN HAEAAQCLVHS	
HC5	DTVKMREFQEDPEMLMDL MYRIAKSYQAS PDLRLTWLQNMAEKHTKKKCY TEAAMCLVHA	
SH3		
HC2A	TALVAEYL TRKGV-----FRQGCTAFRVTITPN	
KIAA	TALVAEYL TRKEA-----VQWEPPLLPHSHSACLRRSRGGVFRQGCTAFRVTITPN	
rat	TALVAEYL TRKEAD-----LALQREPPVPFPYSHTSCQRKSRGGMFRQGCTAFRVTITPN	
HC4	AALVAEFL HRKKL-----FPNGCSAFKKITPN	
HC1	AALIAEYL KRGYWKVEKICTASLLSEDPHPCDSNSLLTTPSGGSMFSGWPAFLSITPN	8.1/8.2
HC3	AALVAEYL SMLED-----RKYLPGVCVTFQNISSN	
HC5	AALVAEYL SMLED-----HSYLPVGSVSFQNISSN	
HC2A	IDEEASMMEDVGMQD-----VHFNEVDVLMELLEQCADGLWKAERYELIADIYKLIPI	8.1
KIAA	IDEEASMMEDVGMQD-----VHFNEVDVLMELLEQCADGLWKAERYELIADIYKLIPI	
rat	IDEEASMMEDVGMQD-----VHFNEVDVLMELLEQCADGLWKAERLRAGLLTSINSSP	
HC4	IDEEGAMKEDAGMMD-----VHYSEEVLLELLEQCVNGLWKAERYEIISEISKLIGPI	17.1/17.2
HC1	IKEEGAAKEDSGMHD-----TPYNEIILVEQLYMCGEFLWKSEYELIADVKNPIIAV	
HC3	VLEESAVSDDVSPDEEGICSGKYFTESGLVGLLEQAAASF SMAGMYEAVNEVYKVLPI	
HC5	VLEESVVSSEDTLSPDEGDGVCAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKVLPI	
ITAM ITAM ITAM ITAM		
HC2A	YEKR RD-----TYFRVAFVFGQAAQYQFTDSETDVE	9.1
KIAA	YEKR R DFERLAHIYD TLH RAYSKVTEVMHSGRRL LGTYFRVAFVFGQAAQYQFTDSETDVE	
rat	SMKSGGTLETHIYD TLH RPYSKVTEVITR-----A-----AGSWDLLPGGLFGQ	
HC4	YENRREFENLTQVYRTLHGAYTKILEVMHTKKRLLG-----TYFRVAFVFGQ	
HC1	FEKQRDFKKLSDIYYDIHRSYLKVAEVVNSEKRLFG-----RYFRVAFVFGQ	
HC3	HEANRDAKKLSTIHGKLQEAFFSKIYHQSTGWERMFG-----TYFRVGFYFG-	9.1
C5	LEAHREFRKLTLTHSKLQRAEDSIVNKH--KRMFG-----TYFRVGFYFG-	
HC2A	-FFEDEDGKEYIYKEPKLTPLSEISQRLCLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA	10.1
KIAA	GFFEDEDGKEYIYKEPKLTPLSEISQRLCLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA	
rat	GFFEDEDGKEYIYKEPKLTPLSEISQRLCLKLYSDKFGSENVKMIQDSGKVNPKDLDSKFA	
HC4	SFFEEEDGKEYIYKEPKLTGLSEISLRLVKLYGEKFGTENVKIIQSDSKVNAKELDPKYA	
HC1	GFFEEEGKEYIYKEPKLTGLSEISQRLCLKLYADKFGADNVKIIQDSNVNPKDLDPKYA	10.1/10.2
HC3	TKFGDLDEQEFVYKEPAITKLAEISHRIEGFYGERFGEDVVEVIKDSNPVDKCKLDPNKA	4.1
HC5	SKFGDLDEQEFVYKEPAITKLPEISHRLEAFYGCFCGAEFVEVIKDSNPVDKCKLDPNKA	
HC2A	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRITILTA	11.1/11.2
KIAA	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRITILTA	
rat	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRITILTA	
HC4	HIQVTVKPYFDDKELTERKTEFERNHNISRFVFEAPYTLGKKQGCIEEQCKRRITILT	18.1
HC1	YIQVTVVTPFFEEKEIEDRKTD FEMHNNINRFVETPFTLSGKKHGGVAEQCKRRITILT	
HC3	YIQITYVEPYFDTYEMKDRITYFDKNYNLRRFMYCTPFTLDGRAHGEHQFRRKRTILT	
HC5	YIQITFVEPYFDEYEMKDRVITYFEKNFNLRRFMYTTPFTLEGRPRGELHEQYRRNTVLT	

FIG. 6B (cont.)

		Coiled-Coil 1	Ref
HC2A	IHCFFPYVKKRIPVMYQHHTDLNP	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLGQSV	
KIAA	IHCFFPYVKKRIPVMYQHHTDLNP	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLGQSV	
rat	IHCFFPYVKKRIPVMYQHHTDLNP	IEVAIDEMSKKVAELHQLCSSAEVDMIKLQLKLGQSV	
HC4	SNSFFPYVKKRIPINCEQQINLKP	IDGATDEIKDKTAELOKLCSSSTDVDMIQQLKLGQWV	
HC1	SHLFFPYVKKRIQVISQSSTELNP	IEVAIDEMSRKVSELNQLCTMEEVDMISLQLKLGQSV	
HC3	SHAFPIKTRVNVTHKEEIIILTP	IEVAIEDMQKKTQELAFATHQDPADPKMLQMVLGQSV	11.1
HC5	MHAFPIKTRISVIQKEEFVLTP	IEVAIEDMKKKTLLQAVAINQEPDAKMLQMVLGQSV	
		Coiled-Coil 2	
HC2A	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFROFVEACGQALAVNERLIKEDQLE		11.1/12.1
KIAA	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFROFVEACGQALAVNERLIKEDQLE		
rat	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFROFVEACGQALAVNERLIKEDQLE		
HC4	SVQVNAGPLAYARAFLLDNDQASKYPPKKVSELKDMFRKFIQACSI ALELNERLIKEDQVE		
HC1	SVKVNAGPMAYARAFLEETNAKKYPDNQVKLLKEIFROFADACGQALDVNERLIKEDQLE		
HC3	GTTVNQGPLEVAQVFLSEIPSDPKLFRHHNKLRLCFKDFTKRCEDALRKKNKSLIGPVQKE		
HC5	GATVNQGPLEVAQVFLAEIPADPKLYRHHNKLRLCFKEFIMRCGEAVEKNKRLITADQRE		
		Coiled-Coil 2	
HC2A	YQEEMKANYREMAKELSEIMHEQICPLEEKTS-VLPNSLHIFNAISGTPSTMTVHGMTSS		
KIAA	YQEEMKANYREMAKELSEIMHEQIC-----		
rat	YQEEMKANYREIRKELSDIIVPRICPGEDKRATKFP AHLQRHQ RDTNKHSGSRVDOFILS		
HC4	YHEGLKSNFRDMVKELSDIIEHQILQEDTMHSPWMSNTLHVFC AISGTSSDRGYGSPRYA		
HC1	YQEELRSHYKDMSELSTVMNEQITGRDDLK---RGVDQTC TRVISKATPALPTVSISS		19.1
HC3	YQRELG---KLSS-----PZ-----		
HC5	YQRELKKNYNKLKENLRPMIERKIPELYKPIFRVESQKRDSFHRSSFRKCETQLSQGSZ-		
		PBM	
HC2A	SSVVZ-----		
KIAA	-----		
rat	CVTLPHPEPHVGTCTFVMCKLRTTFRANHWFCQAQEEAMNGREKEPWTVI FNSRFYRSWGK		
HC4	EVL-----		
HC1	SAEVZ-----		
HC3	-----		
HC5	-----		
HC2A	-----		
KIAA	-----		
rat	VHIFF		
HC4	-----		
HC1	-----		
HC3	-----		
HC5	-----		

FIG. 6B (cont.)

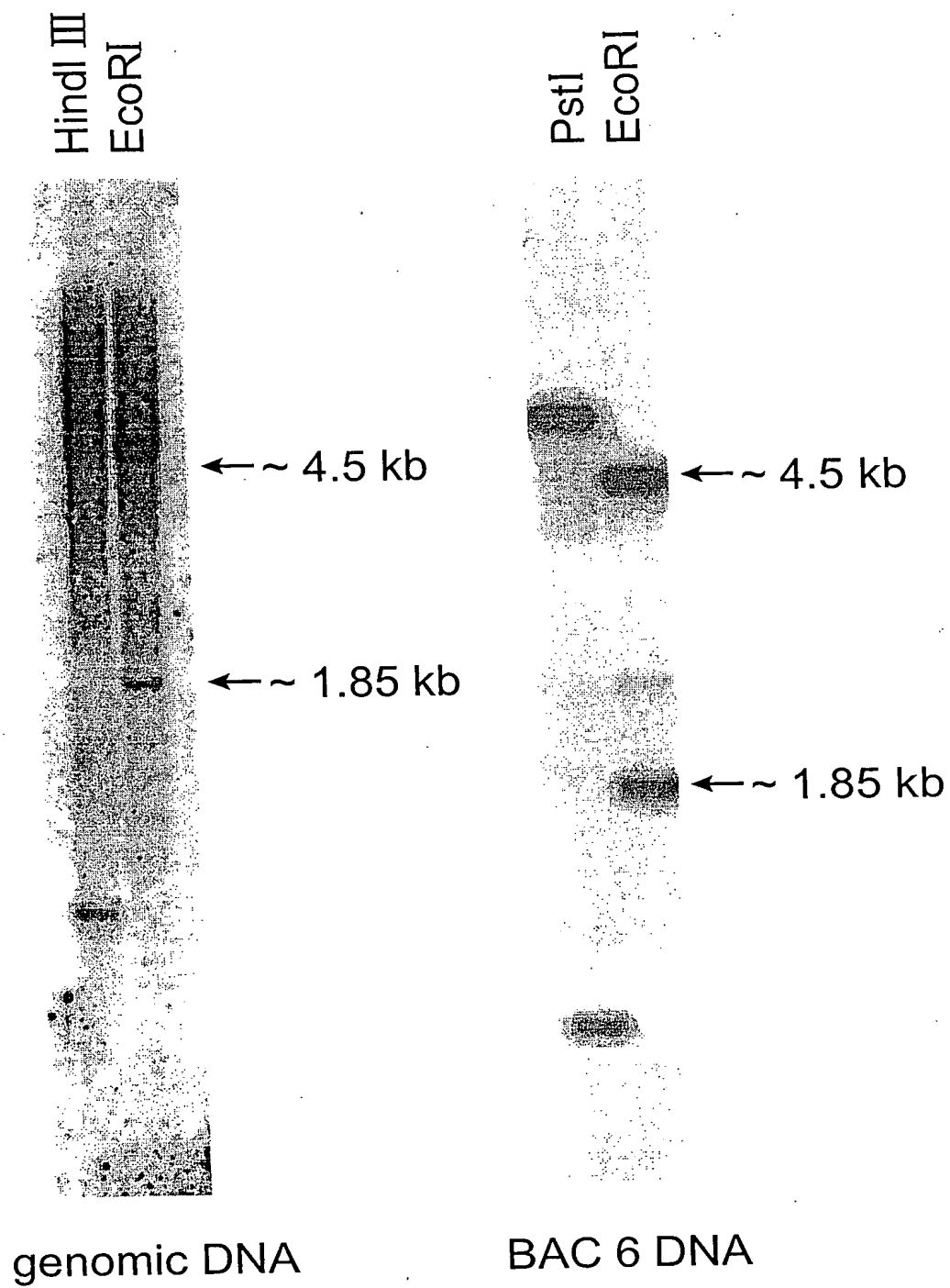


FIG. 7

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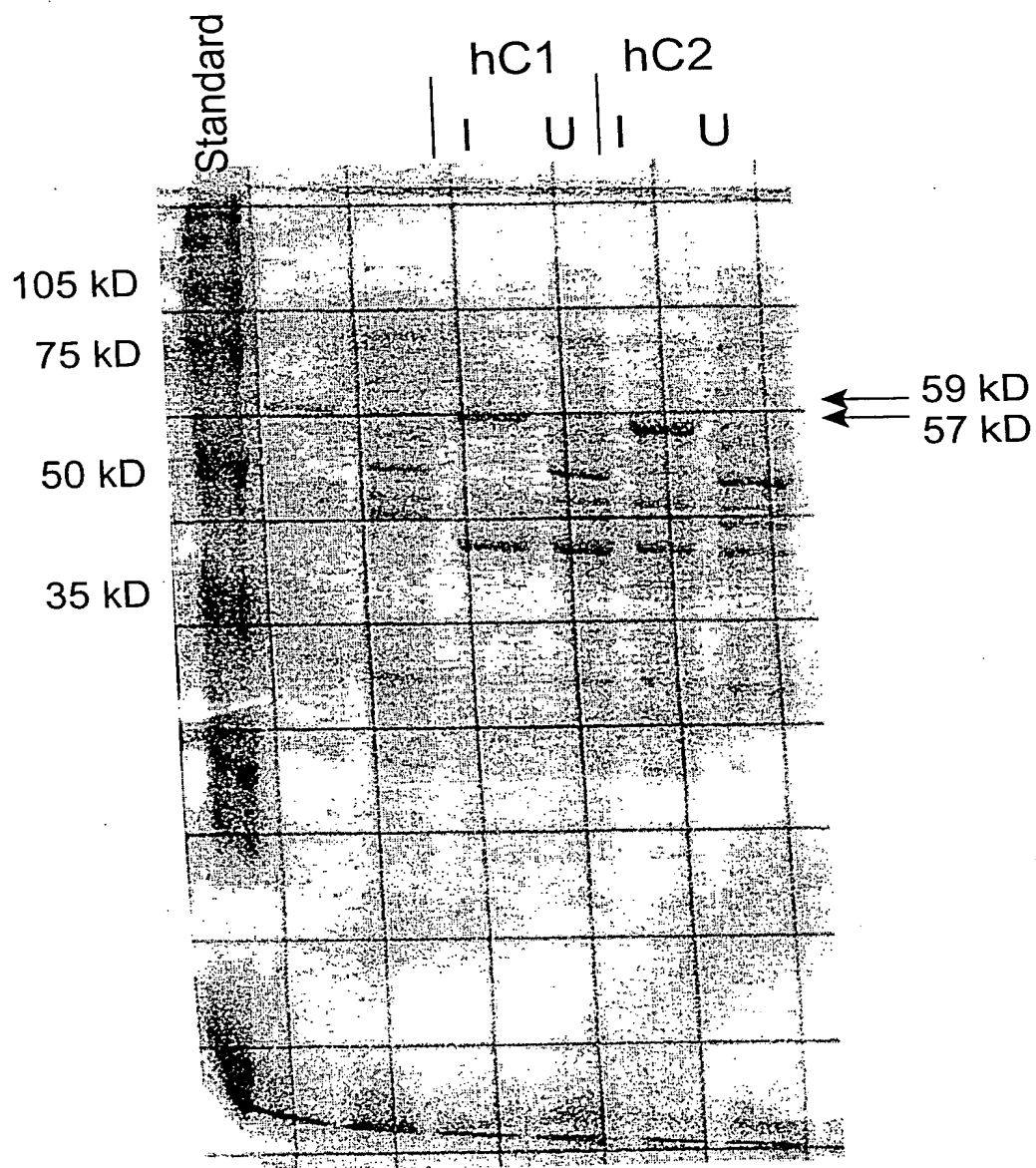


FIG. 8

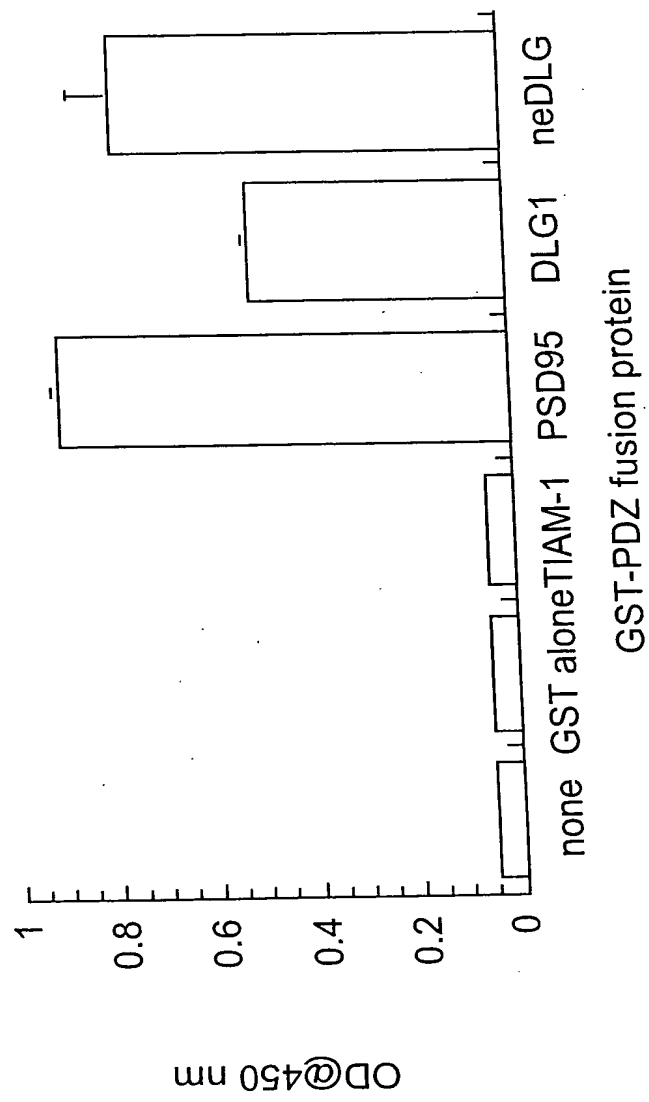


FIG. 9A

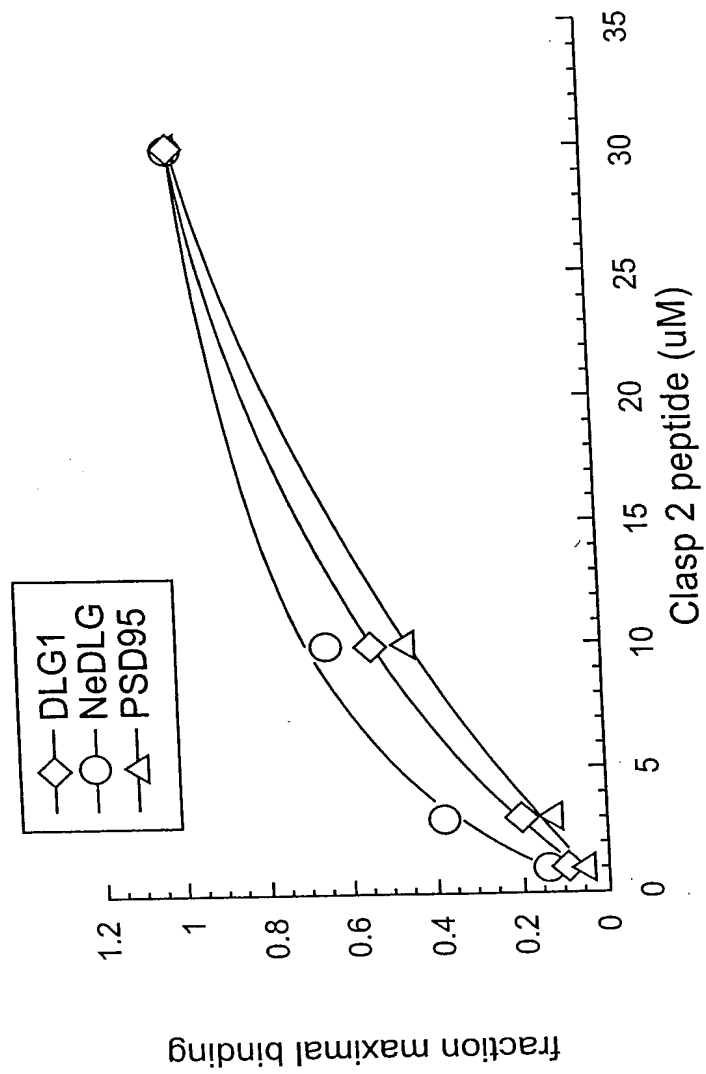


FIG. 9B

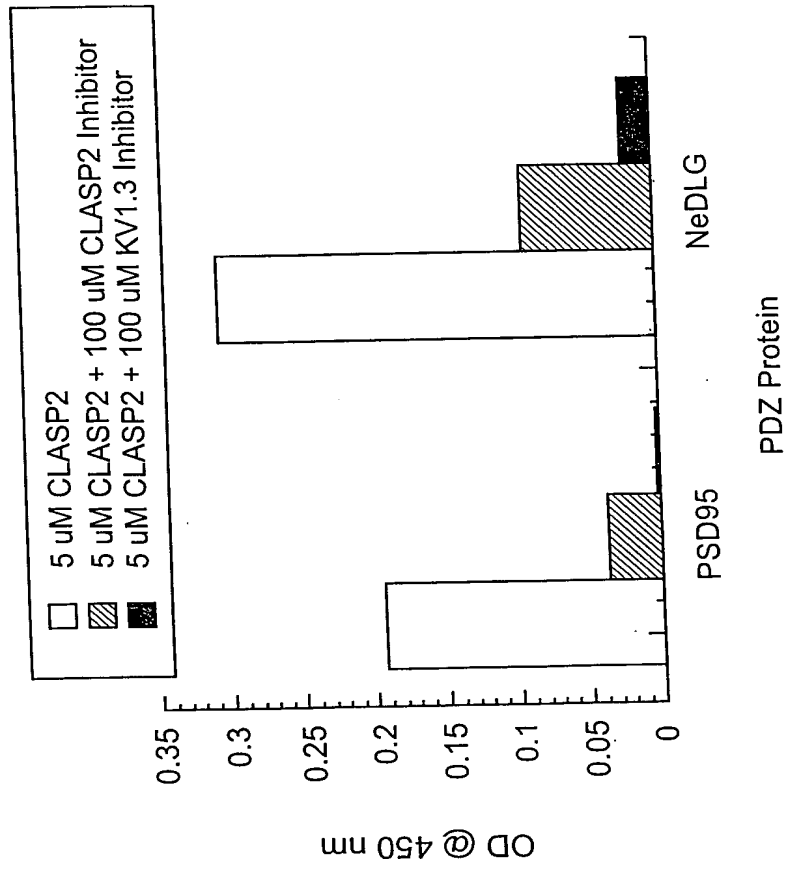


FIG. 9C

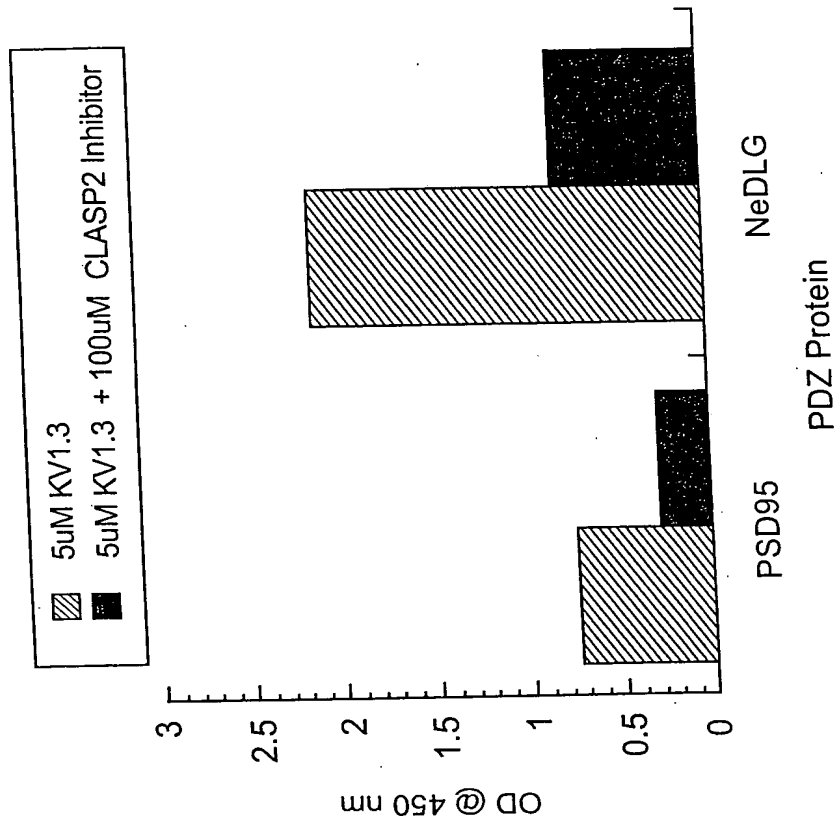


FIG. 9D

	10	20	30	40	50	60	70	80
1	AATTGTAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG	GCCCCCCTC	GAGGTCGACG	GTATCGATAA	GCTTGATATC 80
81	GAATTCGGCA	CGAGTTTTAC	ACCATCACCA	AAACCCAGAA	TTTTATGATG	AGATTAAAT	AGAGTTGCC	ACTCAGCTGC 160
161	ATGAAAAGCA	CCACCTGTTG	CTCACATTCT	TCCATGTCTAG	CTGTGACAC	TCAAGTAAAG	GAAGCAGCAA	GAAGAGGGAT 240
241	GTCGTTGAAA	CCCAAGTTGG	CTACTCCTGG	CTTCCCTCC	TGAAAGACGG	AAGGGTGGTG	ACAAGCCGAC	AGCACATCCC 320
321	GGTCTCGGCG	AACCTTCCTT	CGGGCTATCT	TGGCTACCAA	GAGCTTGGGA	TGGGCAGGCA	TTATGGTCCG	GAATTAAT 400
401	GGGTAGATGG	AGGCAAGCCA	CTGCTGAAAA	TTTCCACTCA	TCTGGTTTCT	ACAGGGATAC	TCAGGATCAG	CATTTACATA 480
481	ATTTTTTCCA	GTACTGTCTAG	AAAACCGAAT	CTGGAGCCCA	AGCCTTAGGA	AACGAACTTG	TAAAGTACCT	TAAGAGTCTG 560
561	CATGCCGATGG	AAGGCCACGT	GATGATCGCC	TTCTTGCCCA	CTATCCTAAA	CCAGCTGTTC	CGAGTCCCTA	CCAGAGCCAC 640
641	ACAGGAAGAA	GTCGCGGTTA	ACGTGACTCG	GGTCATTAT	CATGTGGTTG	CCCAGTGCCA	TGAGGAAGGA	TTGGAGAGCC 720
721	ACTTGAGGTC	ATATGTTAAG	TACGCGTATA	AGGCTGAGCC	ATATGTTGCC	TCTGAATACA	AGACAGTGCA	TGAAGAACTG 800
801	ACCAAATCCA	TGACACGAT	TCTCAAGCCT	TCTGCCGATT	TCTTCACCAG	CAACAACTA	CTGAGGTACT	CATGGTTTTT 880
881	CTTTGATGTA	CTGATCAAAT	CTATGGCTCA	GCATTGATA	GAGAACTCCA	AAGTTAAGTT	GCTGCCAAAC	CAGAGATTTT 960
961	CTGCATCCTA	TCAATCATGCA	GCGGAAACCG	TTGTAATAT	GCTGATGCCA	CACATCACTC	AGAAGTTTGG	AGATAATCCA 1040
1041	GAGGCATCTA	AGAACGCGAA	TCATAGCCTT	GCTGTCTTCA	TCTAAGAGATG	TTTCACCTTC	ATGGACAGGG	GCTTTGTCTT 1120
1121	CAAGCAGATC	AACAACCTACA	TTAGCTGTTT	TGCTCCTGGA	GAGCCAAAGA	CCCTCTTTGA	ATACAAGTTT	GAATTTCTCC 1200
1201	GTGTAGTGTG	CAACCATGAA	CATTATATTC	CGTTGAACCT	ACCAATGCCA	TTTGGAAGAG	GCAGGATTTCA	AAGATACCAA 1280
1281	GACCTCCAGC	TTGACTACTC	ATTAACAGAT	GAGTTCTGCA	GAACCACTT	CTTGGTGGGA	CTGTACTGTA	GGGAGGTGGG 1360
1361	GACAGCCCTC	CAGGAGTTCC	GGGAGGTCCG	TCTGATCGCC	ATCAGTGTGC	TCAAGAACCT	GCTGATAAAG	CATTCTTTTG 1440
1441	ATGACAGATA	TGCTTCAAGG	AGCCATCAGG	CAAGGATAGC	CACCTCTTAC	CTGCCCTCTG	TTGGTCTGCT	CCCTGGCTCT 1520
1521	GTCCAGCGGA	TCAATGTGAG	GGATGTGTCA	CCCTTCCCTG	TGAACGCGGG	CATGACCGTG	AAGGATGAAT	CCCTGGCTCT 1600
1601	ACCAGCTGTG	AATCCGCTGG	TGACGCCGCA	GAAGGGAAGC	ACCTTGGACA	ACAGCTGCA	CAAGGACCTG	CTGGCGGCCA 1680
1681	TCTCCGGCAT	TGCTTCTCCA	TATACAACCT	CAACTCCAAA	CATCAACAGT	GTGAGAAATG	CTGATTCGAG	AGGATCTCTC 1760
1761	ATAAGCACAG	ATTCCGGTAA	CAGCCTTCCA	GAAGGAATA	GTGAGAAAG	CAATTCCCTG	GATAAGCACC	AACAAGTAGT 1840
1841	CACATTGGGA	AATTCGCTGG	TTCGCTGTGA	TAACTTGAC	CAGTCTGAGA	TTAAGAGCCT	ACTGATGTGT	TTCTCTTACA 1920
1921	TCCTAAAGAG	CATGTCTGAT	GATGCTTTGT	TTACATATTG	GAACAAGGCT	TCAACATCTG	AACTTATGGA	TTTTTTTACA 2000
2001	ATATCTGAAG	TCTGCCTGCA	CCAGTTCCAG	TACATGGGGA	AGCGATACAT	AGCCAGGAAC	CAGGAGGGGT	TGGGACCCAT 2080
2081	AGTTCATGAT	CGAAAGTCTC	AGACATTGCC	TGTTTCCCGT	AACAGAACAG	GAATGATGCA	TGCCAGATTG	CAGCAGCTGG 2160
2161	GCAGCCTGGA	TAACCTCTCT	ACTTTTAACC	ACAGCTATGG	CCACTCGGAC	GCAGATGTTT	TGCACCAAGT	ATTACTTGAA 2240
2241	GCCAACATTG	CTACTGAGGT	TTGCCCTGACA	GCTCTGGACA	CGCTTCTCT	ATTTACATTG	CGCTTTAAGA	ACCAGCTCCT 2320
2321	GGCCGACCAT	GGACATAATC	CTCTCATGAA	AAAAGTTTTT	GATGTCTACC	TGTGTTTTCT	TCAAAAACAT	CAGTCTGAAA 2400
2401	CGGCTTTTAA	AAATGCTTTC	ACTGCCCTTAA	GGTCCCTAAT	TTATAAGTTT	CCCTCAACAT	TCTATGAAGG	GAGAGCGGAC 2480
2481	ATGTGTGCGG	CTCTGTGTTA	CGAGATTCTC	AAGTGGCTGA	ACTCCAAGCT	GAGCTCCATC	AGGACGGAGG	CCTCCAGCT 2560
2561	GCTCTACTTC	CTGATGAGGA	ACAACCTTGA	TTACACTGGA	AAGAAGTCTT	TGTCCGGGAC	ACATTGTCAA	GTCTCATAT 2640
2641	CTGTGAGCCA	GCTGATAGCA	GACGTTGTTG	GCATTGGGGA	AACAGATTTC	CAGCAGTCCC	TGTCCATCAT	CAACAACCTG 2720
2721	GCCAACAGTG	ACCGGCTTAT	TAAGCACACC	AGCTTCTCCT	CTGATGTGAA	GGACTTAACC	AAAAGGATAC	GCACGGGTCT 2800
2801	AATGGCCACC	GCCCAGATGA	AGGAGCATGA	GAACGACCCA	GAGATGCTGG	TGGACCTCCA	GTACAGCCTG	GCCAAATCCT 2880
2881	ATGCCAGCAG	GCCCGAGCTC	AGGAAGACGT	GGCTCGACAG	CATGGCCAGG	ATCCATGTCA	AAAATGGCGA	TCTCTCAGAG 2960
2961	GCAGCAATGT	GCTATGTCCA	CGTAACAGCC	CTAGTGGCAG	AATATCTCAC	ACGGAAGGCG	GTGTTTAGAC	AAGGATGCA 3040
3041	CGCCTTCAGG	GTCATTACCC	CAAACATCGA	CGAGGAGGCC	TCCATGATGG	AAGACGTGGG	GATGCAGGAT	GTCCATTTC 3120
3121	ACGAGGATGT	GCTGATGGAG	CTCCTTGAGC	AGTGCGCAGA	TGGACTCTGG	AAAGCCGAGC	GCTACGAGCT	CATCGCCGAC 3200
3201	ATCTACAAAC	TTATCATCCC	CATTTATGAG	AAGCGGAGGG	ATTTCTTTGA	AGATGAAGAT	GGAAAGGAGT	ATATTTACAA 3280
3281	GGAAACCCAAA	CTCACACCGC	TGTCGGAAAT	TTCTCAGAGA	CTCCTTAAAC	TGTACTCGGA	TAAATTTGGT	TCTGAAAATG 3360
3361	TCAAAATGAT	ACAGGATTCT	GGCAAGGTCA	ACCCTAAGGA	TCTGGATTCT	AAGTATGCAT	ACATCCAGGT	GACTCACGTC 3440
3441	ATCCCTTCTT	TTGACGAAAA	AGAGTTGCAA	GAAGGAAAAA	CAGAGTTTGA	GAGATCCAC	AACATCCGCC	GCTTCATGTT 3520
3521	TGAGATGCCA	TTTACGCAGA	CCGGGAAGAG	GCAGGGCGGG	GTGGAAGAGC	AGTGCAAAAC	GCGCACCATC	CTGACAGCCA 3600
3601	TACACTGCTT	CCCTTATGTG	AAGAAGCGCA	TCCCTGTCTAT	GTACCAAGCA	CACACTGACC	TGAACCCCAT	CGAGGTGGCC 3680
3681	ATTGACGAGA	TGAGTAAGAA	GGTGGCGGAG	CTCCGCGAGC	TGTGCTCCTC	GGCCGAGGTG	GACATGATCA	AACTGCAGCT 3760
3761	CAAACTCCAG	GGCAGCGTGA	GTGTTGAGGT	CAATGCTGGC	CCACTAGCAT	ATGCGCGAGC	TTTCTTAGAT	GATACAAACA 3840
3841	CAAAAGCGATA	TCTTGACAAT	AAAGTGAAGC	TGCTTAAAGGA	AGTTTTCAGG	CAATTGTGTT	AAGCTTGGCG	TTAAGCCCTT 3920
3921	CGCGTAAACG	AACGTCTGAT	TAAAGAAGAC	CAGCTCGAGT	ATCAGGAAGA	AATGAAAGCC	AACTACAGGG	AAATGGCGAA 4000
4001	GGAGCTTTCT	GAAATCATGC	ATGAGCAGAT	CTGCCCCCTG	GAGGAGAAGA	CGAGCGTCTT	ACCGAATTCC	CTTCACATCT 4080
4081	TCAACGCCAT	CAGTGGGACT	CCAACAAGCA	CAATGGTTCA	CGGGATGACC	AGCTCGTCTT	CGGTGCTGTT	ATTACATCTC 4160
4161	ATGGCCCGTG	TGTGGGGACT	TGCTTTGTCA	TTTGCAAACT	CAGGATGCTT	TCCAAAGCCA	ATCACTGGGG	AGACCGAGCA 4240
4241	CAGGAGGAGC	CAAGGGGAAG	GGGAGAGAAA	GGAAATAAAG	AACAACGTTA	TTTCTTAACA	GACTTTCTAT	AGGAGTTGTA 4320
4321	AGAAGGTGCA	CATATTTTTT	TAAATCTCAC	TGGCAATATT	CAAAGTTTTT	ATTGTGCTTT	AACAAAGTGT	TGGTAGACAC 4400
4401	TCTTGAGCTG	GACTTAGATT	TTATTCTTCC	TTGCAGAGTA	GTGTTAGAA	AGATGGCCTA	CAGAAAAAAA	AGGTTCTGGG 4480
4481	ATCTACATGG	CAGGGAGGGC	TGCACTGACA	TTGATGCTGT	GGGGACCTTT	TGCTCGAGT	CGTGCCGGAA	ATCTGATCGT 4560
4561	AATCAGGGTA	CAGAACTTAC	TAGTTTTGTC	TAGGAGTATG	TTGATGACT	AGGATTGTG	CTATTATCTC	ATTCAACAAC 4640
4641	ATAGAGCAAG	AATAGTGAGC	TAACTGAGCT	AGACACTCAA	TTAATCCGCT	ACTGGCTTCA	AGTCAGAACT	TTGTCTTAA 4720
4721	TCATCGACTC	CGGGACGGTC	ATATATGTAT	TACATTTCTA	CATTTTAAAT	ACTCACATGG	GCTTATGCAT	TAAGTTTAA 4800
4801	TGTGATAAAT	TTGTGCTGGT	CCAGTATATG	CAATACACTT	TAATGGTTTA	TTCTTGTCAT	AAAAATGTGC	AATATGGAGA 4880
4881	TGTATACAAG	TCTTTACT						4898

FIG.10A

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	10	20	30	40	50	60	70	80
1	MEGHVMIAFL	PTILNQLFRV	LTRATQEEVA	VNVTRVIIHV	VAQCHEEGLE	SHLSRYVKYA	YKAEPYVASE	YKTVHEELTK 80
81	SMTTILKPSA	DFLTSNKLLR	YSWFFFDVLI	KSMAQH LIEN	SKVKLLRNQR	FPASYHHAAE	TVVNMI MPHI	TQKFGDNPEA 160
161	SKNANHSLAV	FIKRCFTFMD	RGFVFKQINN	YISCFAPGDP	KTLFEYKFEF	LRVVCNHEHY	IPLNLPMPFG	KGRIQRYQDL 240
241	QLDYSLTDEF	CRNHFLVGLL	LREVG TALQE	FREVRLIAIS	VLKNLLIKHS	FDDRYASRSH	QARIATLYLP	LFGLLIENVQ 320
321	RINVRDVSPF	PVNAGMTVKD	ESLALPAVNP	LVT PQKGSTL	DNSLHKDLLG	AISGIASPYT	TSTPNINSVR	NADSRGSLIS 400
401	TDSGNSLPER	NSEKSNSLDK	HQQSSTLGNS	VVRCDKLDQS	EIKSLIMCFL	YILKSMSDDA	LFTYWNKAST	SELMDEFTIS 480
481	EVCLHQFQYM	GKRYIARNQE	GLGP IVHDRK	SQTLFVSRNR	TGMMHARLQQ	LGSLDNSLTF	NHSYGHSDAD	VLHQSLLEAN 560
561	IATEVCLTAL	DTLSLFTLAF	KNQLLADHGH	NPLMKKVFDV	YLCFLQKHQS	ETALKNVETA	LRSLYKFPS	TFYEGRADMC 640
641	AALCYEILKC	CNSKLS SIRT	EASQLLYFLM	RNNFDYTGKK	SEVRTHLQVI	ISVSQLIADV	VGIGETRFOQ	SLSIINN CAN 720
721	SDRLIKHTSF	SSDVKDLTKR	IRTVLMATAQ	MKEHENDPEM	LVDLQYSLAK	SYASTPELRK	TWLD SMARIH	VKNGDLSEAA 800
801	MCYVHV TALV	AEYLTRKGVF	RQGCTAFRVI	TPNIDEEASM	MEDVGMQDVH	FNEDVLMELL	EQCADGLWKA	ERYELIADIY 880
881	KLIPIIYEKR	RDFEDEDGK	EYIYKEPKLT	PLSEISQRLL	KLYSDKFGSE	NVKMIQDSGK	VNPKDLDSKY	AYIQVTHVIP 960
961	FFDEKELQER	KTEFERSHNI	RRFMFEMPFT	QTGKRQGGVE	EQCKRRRTILT	AIHCFPYVKK	RIPVMYQHHT	DLNPIEVAID 1040
1041	EMSKKVAELR	QLCSSAEVDM	IKLQLKLQGS	VSVQVNAGPL	AYARAF LDDT	NTKRYPDNKV	KLLKEVERQF	VEACGQALAV 1120
1121	NERLIKEDQL	EYQEEMKANY	REMAKELSEI	MHEQICPLEE	KTSVLPNSLH	IFNAISGTPT	STMVHGTTSS	SSVV 1195

FIG. 10A (cont.)

	10	20	30	40		50	60	70	80
1	AATTGTAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG	CCCCCCCCCTC	GAGGTCGACG	GTATCGATAA	GCTTGATATC	80
81	GAATTCGGCA	CGAGTTTTAC	ACCATCACCA	AAACCCAGAA	TTTTATGATG	AGATTAAAT	AGAGTTGCC	ACTCAGCTGC	160
161	ATGAAAAGCA	CCACCTGTTG	CTCACATTCT	TCCATGTTCAG	CTGTGACAAC	TCAAGTAAAG	GAAGCAGGAA	GAAGAGGGAT	240
241	GTGCTTGAAA	CCCAAGTTGG	CTACTCCTGG	CTTCCCCTCC	TGAAAGACGG	AAGGGTGGTG	ACAAGCGAGC	AGCACATCCC	320
321	GGTCTCGCGG	AACCTTCCTT	CGGGCTATCT	TGGCTACCAA	GAGCTTGGGA	TGGGCAGGCA	TTATGGTCCG	GAAATTAAT	400
401	GGGTAGATGG	AGGCAAGCCA	CTGCTGAAAA	TTTCCACTCA	TCTGTGTTCT	ACAGGGATAC	TCAGGATCAG	CATTTACATA	480
481	ATTTTTCCTA	GTACTGTGAG	AAAACCGAAT	CTGGAGCCCA	AGCCTTAGGA	AACGAACTTG	TAAAGTACCT	TAAGAGTCTG	560
561	CATGCGATGG	AAGGCCACGT	GATGATCGCC	TTCTTGCCCA	CTATCCTAAA	CCAGCTGTTC	CGAGTCCTCA	CCGAGGCCAG	640
641	ACAGGAAGAA	GTCGCGGTTA	ACGTGACTCG	GGTCATTATT	CATGTGGTTG	CCCAGTGCCA	TGAGGAAGGA	TTGGAGAGCC	720
721	ACTTGAGGTC	ATATGTTAAG	TACGCGTATA	AGCGTGAGCC	ATATGTTGCC	TCTGAATACA	AGACAGTGCA	TGAAGAACTG	800
801	ACCAAAATCCA	TGACCACGAT	TCTCAAGCCT	TCTGCCGATT	TCTTCACCAG	CAACAAACTA	CTGAGTACT	CATGTTTTTT	880
881	CTTTGATGTA	CTGATCAAAT	CTATGGCTCA	GCATTTGATA	GAGAACTCCA	AAGTTAAGTT	GCTGCCAAAC	CAGAGATTTC	960
961	CTGCATCCTA	TCATCATGCA	GCGGAAACCG	TTGTAATAT	GCTGATGCCA	CACATCACTC	AGAAGTTTGG	AGATAATCCA	1040
1041	GAGGCATCTA	AGAACGCGAA	TCATAGCCTT	GCTGTCTTCA	TCAAGAGATG	TTTCACCTTC	ATGGACAGGG	GCTTTGTCTT	1120
1121	CAAGCAGATC	AACAACATA	TTAGCTGTTT	TGCTCTGGGA	GACCCAAAGA	CCCTCTTTGA	ATACAAGTTT	GAATTTCTCC	1200
1201	GTGTAGTGTG	CAACCATGAA	CATTATATTC	CGTTGAACTT	ACCAATGCCA	TTTGGAAGAG	GCAGGATTCA	AAGATACCAA	1280
1281	GACCTCCAGC	TTGACTACTC	ATTAACAGAT	GAGTTCTGCA	GAAACCACTT	CTTGGTGGGA	GCTGATAAAG	CATTCTTTTG	1440
1361	GACAGCCCTC	CAGGAGTTCC	GGGAGGTCGG	TCTGATCGCC	CACCTCTTAC	CTGCCCTGCT	TTGGTCTGCT	GATTGAAAA	1520
1441	ATGACAGATA	TGCTTCAAGG	AGCCATCAGG	CAAGGATAGC	TGAACCGGGG	CATGACCGTG	AAGGATGAAT	CCCTGGCTCT	1600
1521	GTCCAGCGGA	TCATGTGTAG	GGATGTGTCA	CCCTTCCCTG	ACCGCTGGACA	ACAGCCTGCA	CAAGGACCTG	CTGGCGCCCA	1680
1601	ACCAGCTGTG	AATCCGCTGG	TGACGCGCCA	GAAGGGAAGC	CATCAACAGT	GTGAGAAATG	CTGATTCGAG	AGGATCTCTC	1760
1681	TCTCCGCGAT	TGCTTCTCCA	TATACAACCT	CAACTCCAAA	GTGAGAAGAG	CAATTCCCTG	GATAAGCACC	AACAAAGTAG	1840
1761	ATAAGCACAG	ATTCCGGGTA	CAGCCTTCCA	GAAGGAATA	CTCATCTAGA	TTAAGAGCCT	ACTGATGTGT	TTCTCTTACA	1920
1841	CACATTGGGA	AATTCCGTTG	TTGCTGTGTA	TAACTTGAC	GAACAAGGCT	TCAACATCTG	AACCTTATGA	TTTTTTTACA	2000
1921	TCTTAAAGAG	CATGCTGTAT	GATGCTTTGT	TTACATATTG	AGCGATACAT	AGCCAGGAAC	CAGGAGGGGT	TGGGACCCAT	2080
2001	ATATCTGAAG	TCTGCCTGCA	CCAGTTCCAG	TACATGGGGA	AACAGAACAG	GAATGATGCA	TGCCAGATTG	CAGCAGCTGG	2160
2081	AGTTTATGAT	CGAAAGTCTC	AGACATTCCT	ACTTTTAAAC	CCACTCCGAC	GCAGATGTTT	TGCACCCAGT	ATTACTTTGA	2240
2161	GCAGCCTGGA	TAACCTCTCT	ACTTTTAAAC	ACAGCTATGG	CGCTTTCTCT	ATTACATTG	GCGTTTAAAG	ACCAGCTCCT	2320
2241	GCCACATTTG	CTACTGAGGT	TTGCCTGACA	GCTCTGGACA	GATGCTTACC	TGTGTTTTCT	TCAAAAACAT	CAGTCTGAAA	2400
2321	GGCCGACCAT	GGACATAATC	CTCTCATGAA	AAAGTTTCTT	TTATAAGTTT	CCCTCAACAT	TCTATGAAGG	GAGAGCGGAG	2480
2401	CGGCTTTTAA	AAATGTCTTC	ACTGCCTTAA	GGTCCCTTAA	ACTTCCAACT	GAGCTCCATC	AGGACGGAGT	CCTCCAGGCT	2560
2481	ATGTGTGCGG	CTCTGTGTTA	CGAGATTCTC	AAGTGTCTGA	AAGAAGTCTT	TTGTCCGGAC	ACATTTGCAA	GTCTATCATAT	2640
2561	GCTCTACTTC	CTGATGAGGA	ACAACTTTGA	TTAACTTGGA	AACCAGATTG	CAGCAGTCCC	TGTCCATCAT	CAACAACCTG	2720
2641	CTGTFCAGCA	GCTGATAGCA	GACGTTGTTG	GCATTGGGGA	CTGATGTGAA	GGACTTAACC	AAAAGGATAC	GTACAGCCTG	2800
2721	GCCAAACAGT	ACCGGCTTAT	TAAGCACACC	AGCTTCTCCT	GAGATGCTGG	TGGACCTCCA	AAAATGGCGA	TCTCTCAGAG	2880
2801	AATGGCCACC	GCCCAGATGA	AGGAAGACGT	GGCTCGACAG	CATGCCCCAG	ATCCATGTCA	AAAATGGCGA	TCTCTCAGAG	2960
2881	ATGCCAGCAC	GCCCGAGCTC	AGGAAGACGT	GGCTCGACAG	AAATATCTAC	ACGGAAGGCG	GTGTTTAGAT	GTCCATTTC	3040
2961	GCAGCAATGT	GCTATGTCCA	CGTAACAGCC	CTAGTGGCAG	TCCATGATGG	AAGACGTGGG	GATGCGAGAT	GTCCATTTC	3120
3041	CGCCTTCAGG	GTCTATTACC	CAACATCGA	CGAGGAGGCC	TGGACTCTGG	AAAGCCGAGC	GCTACGAGCT	CATCCCGCAG	3200
3121	ACGAGGATGT	GCTGATGGAG	CTCCTTGAGC	AGTGCGCAGA	ATTTCTTTGA	AGATGAAGAT	GGAAGGAGT	ATATTACAA	3280
3201	ATCTACAAC	TTATCATCCC	CATTATGAG	AAGCGGAGGG	CTCCTTAAAC	TGTACTCGGA	TAAATTTGGT	TCTGAAAATG	3360
3281	GGAACCCAAA	CTCACACCGC	TGTCGGAAT	TTCTCAGAGA	TCTGGATTCT	AAGTATGCAT	ACATCCAGGT	GACTCAGCTC	3440
3361	TCAAAATGAT	ACAGGATTCT	GGCAAGGTCA	ACCCTAAGGA	CAGAGTTTGA	GAGATCCCAC	AACATCCGCG	GCTTCATGTT	3520
3441	ATCCCTTCTT	TTGACGAAAA	AGAGTTGCAA	GAAAGGAAAA	GTGGAAGAGC	AGTGCAAACG	CGGCACCATC	CTGACAGCCA	3600
3521	TGAGATGCCA	TTTACGCAGA	CCGGGAAGAG	GCAGGGCCGG	GTACCAGCAC	CACACTGACC	TGAACCCCAT	CGAGGTGGCC	3680
3601	TACACTGCTT	CCCTTATGTG	AAGAAGCGCA	TCCCTGTCTAT	TGTGCTCCTC	GGCCGAGGTG	GACATGATCA	AACTGCAGCT	3760
3681	ATTGACGAGA	TGAGTAAGAA	GGTGGCGGAG	CTCCGCGCAG	CCACTAGCAT	ATGCGCGAGC	TTTCTTAGAT	GATACAAACA	3840
3761	CAAACCTCCG	GGCAGCGTGA	GTGTTCAAGT	CAATGCTGGC	AGTTTTTCAGG	CAATTTGTGG	AAGCTTGCGG	TCAAGCCTTA	3920
3841	CAAAGCGATA	TCCTGACAA	AAAGTGAAGC	TGCTTAAGGA	ATCAGGAAGA	AATGAAAGCC	AACACAGGG	AAATGGCGGA	4000
3921	GCGGTAAACG	AACGCTCTGAT	TAAAGAAAGC	CAGCTCGAGT	GAGGAGAAGA	CGAGCGTCTT	ACCGAATTCC	CTTCACATCT	4080
4001	GGAGCTTTCT	GAAATCATGC	ATGACGAGAT	CTGCCCCCTG	CGGGATGACC	AGCTCGTCTT	CGGTCTGTGT	ATTACATCTC	4160
4081	TCAACGCCAT	CAGTGGGACT	CCAACAAGCA	CAATGGTTCA	CAGGATGCTT	TCCAAAGCCA	ATCACTGGGG	AGACCGAGCA	4240
4161	ATGGCCCGTG	TGTGGGGAAT	TGCTTTGTCA	TTTGCAAACT	AACAACGTTA	TTTCTTAAAC	GACTTTCTAT	AGGAGTTGTA	4320
4241	CAGGGAGGAC	CAAGGGGAAG	GGGACAGAAA	GGAAATAAAG	CRAAGTTTTC	ATTGTGTCTT	AACAAAGGTG	TGGTAGACAC	4400
4321	AGAAGGTGCA	CATATTTTTT	TAAATCTCAC	TGGCAATATT	GTGTTAGAAT	AGATGGCCTA	CGTGCCGGAA	ATCTGATCGT	4480
4401	TCTTGAGCTG	GACTTAGATT	TTATCTCTCC	TTGCAGAGTA	GGGACCTTTT	TGCCCTCGAT	CGTGCCGGAA	ATCTGATCGT	4560
4481	ATCTACATGG	CAGGGAGGGC	TGCACCTGAC	TTGATGCTCG	TTGTATGACT	AGGATTGTGT	CTATTATCTC	ATTCAACAAC	4640
4561	AATCAGGGTA	CAGAACCTAC	TAGTTTTGTC	TAGGAGTATG	TTAATCCGCT	ACTGGCTTCA	AGTCAGAACT	TTGTCTATTA	4720
4641	ATAGAGCAAG	AATAGTGAGC	TAACTGAGCT	AGACACTCAA	CATTTTAAAT	ACTCACATGG	GCTTATGCAT	TAAGTTTAA	4800
4721	TCATCGACTC	CGGGACGGTC	ATATATGTAT	TACATTCTTA	TAATGGTTTA	TTCTTGTCTAT	AAAAATGTGC	AATATGGAGA	4880
4801	TGTGATAAAT	TTGTGCTGGT	CCAGTATATG	CAATACACTT					4898
4881	TGTATACAAG	TCTTTACT							
	10	20	30	40		50	60	70	80

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	10	20	30	40	50	60	70	80	
1	MEGHVIAFL	PTILNQLFRV	LTRATQEEVA	VNVTRVHHV	VAQCHEEGLE	SHLRSYVKYA	YKAEPYVASE	YKTVHEELTK	80
81	SMTTILKPSA	DFLTSNKLLR	YSWFFFDVLI	KSMAQHLEIN	SKVKLLRNQR	FPASYHHAAE	TVVNMLMPHI	TQKFGDNPEA	160
161	SKNANHSLAV	FIKRCFTFMD	RGFVFKQINN	YISCFAPGDP	KTLFEYKFEF	LRVVCNHEHY	IPLNLPMPFG	KGRIQRYQDL	240
241	QLDYSLTDEF	CRNHFLVGLL	LREVGTAQOE	FREVRLIAIS	VLKNLLIKHS	FDDRYASRSH	QARIATLYLP	LFGLLIENVQ	320
321	RINVRDVSPF	PVNAGMTVKD	ESLALPAVNP	LVTPOKGSTL	DNSLHKDLG	AISGLASPYT	TSTPNINSVR	NADSRGSLIS	400
401	TDSGNSLPER	NSEKSNSLDK	HQSSSTLGNS	VVRCDKLDQS	EIKSLLMCFL	YILKSMSDDA	LEFTYWNKAST	SEIMDFFTIS	480
481	EVCLHQFQYM	GKRYIARNQE	GLGPIVHDRK	SQTLFVSRNR	TGMMHARLQQ	LGSLDNSLTF	NHSYGHSDAD	VLHQSLLEAN	560
561	IATEVCLTAL	DTLSLFTLAF	KNQLLADHGH	NPLMKKVEDV	YLCFLQKHQS	ETALKNVFTA	LRSLIYKFPS	TFYEGRADMC	640
641	AALCYEILKC	CNSKLSSIRT	EASQLLYFLM	RNNFDYTGKK	SEVVRTHLQVI	ISVSQLIADV	VGIGETRFQQ	SLSIINNCAN	720
721	SDRLIKHTSF	SSDVKDLTKR	IRTVLMATAQ	MKEHENDPEM	LVDLQYSLAK	SYASTPELRK	TWLDSMARIH	VKNGDLSEAA	800
801	MCYVHVHTALV	AEYLTRKGVF	RQCCTAFRVI	TPNIDEEASM	MEDVGMQDVH	FNEDVLMELL	EQCADGLWKA	ERYELIADIY	880
881	KLIPIIYEKR	RDFEDEDGK	EYIYKEPKLT	PLSEISQRLI	KLYSDKFGSE	NVKMIQDSGK	VNPKDLDSKY	AYIQVTHVIP	960
961	FFDEKELQER	KTEFERSHNI	RRFMFEMPFT	QTGKRQGGVE	EQCKRRTILT	AIHCFPYVKK	RIPVMYQHHT	DLNPIEVAID	1040
1041	EMSKKVAELR	QLCSSAEVDM	IKLQLKLQGS	VSVQVNAGPL	AYARAFLLDT	NTKRYPDNKV	KLLKEVFRQF	VEACGQALAV	1120
1121	NERLIKEDQL	EYQEEMKANY	REMAKELSEI	MHEQICPLEE	KTSVLPNSLH	IFNAISGTPT	STMVHGMTSS	SSVV	1195
	10	20	30	40	50	60	70	80	

FIG. 10B (cont.)

	10	20	30	40	50	60	70	80
1	AATTGTAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG	CCCCCCCCCTC	GAGGTCGACG	GTATCGATAA	GCTTGATATC 80
81	GAATTCGGCA	CGAGTTTTC	ACCATCACCA	AAACCCAGAA	TTTTATGATG	AGATTAAAT	AGAGTTGCCC	ACTCAGCTG 160
161	ATGAAAAGCA	CCACCTGTTG	CTCACATTCT	TCCATGTCAG	CTGTGACAAC	TCAAGTAAAG	GAAGCACGAA	GAAGAGGAT 240
241	GTGCTTGAAA	CCCAAGTTGG	CTACTCCTGG	CTTCCCTGCC	TGAAAGACGG	AAGGGTGGTG	ACAAGCGAGC	AGCACATCCC 320
321	GGTCTCGGCG	AACCTTCCTT	CGGGCTATCT	TGGCTACCAA	GAGCTTGGGA	TGGGCAGGCA	TTATGGTCCG	GAATTAAT 400
401	GGGTAGATGG	AGGCAAGCCA	CTGCTGAAAA	TTTCCACTCA	TCTGGTTTCT	ACAGGGATAC	TCAGGATCAG	CATTTACATA 480
481	ATTTTGTCCA	GTACTGTGAG	AAAACCGAAT	CTGGAGCCCA	AGCCTTAGGA	AACGAACCTG	TAAAGTACCT	TAAGAGTCTG 560
561	CATGCGATGG	AAGGCCACGT	GATGATCGCC	TTCTTGCCCA	CTATCCTAAA	CCAGCTGTTC	CGAGTCTCTA	CCAGAGCCAC 640
641	ACAGGAAGAA	GTCGCGGTTA	ACGTGACTCG	GGTCATTATT	CATGTGGTTG	CCCAGTGCCA	TGAGGAAGGA	TTGGAGAGCC 720
721	ACTTGAGGTC	ATATGTTAAG	TACGCGTATA	AGGCTGAGCC	ATATGTTGCC	TCTGAATACA	AGACAGTGCA	TGAAGAACTG 800
801	ACCAAATCCA	TGACCACGAT	TCTCAAGCCT	TCTGCCGATT	TCCCTCACCAG	CAACAAACTA	CTGAGGTACT	CATGGTTTTT 880
881	CTTTGATGTA	CTGATCAAA	CTATGGCTCA	GCATTTGATA	GAGAACTCCA	AAGTTAAGTT	GCTGCCAAAC	CAGAGATTC 960
961	CTGCTACCTA	TCATCATGCA	GCGGAAACCG	TTGTAATAT	GCTGATGCCA	CACATCACTC	AGAAGTTTGG	AGATAATCCA 1040
1041	GAGGCACTA	AGAACGCGAA	TCATAGCCTT	GCTGTCTTCA	TCAAGAGATG	TTTCACCTTC	ATGGACAGGG	GCTTTGTCTT 1120
1121	CAAGCAGATC	AACAACATACA	TTAGCTGTTT	TGCTCCTGGA	GACCCAAAGA	CCCTCTTTGA	ATACAAGTTT	GAATTTCTCC 1200
1201	GTGTTAGTGT	CAACCATGAA	CATTATATTC	CGTTGAACCT	ACCAATGCCA	TTTGGAAAAG	GCAGGATTC	AAGATACCAA 1280
1281	GACCTCCAGC	TTGACTACTC	ATTAACAGAT	GAGTTCTGCA	GAACCACTT	CTTGGTGGGA	CTGTTACTGA	GGGAGGTGGG 1360
1361	GACAGCCCTC	CAGGAGTTCC	GGGAGGTCCG	TCTGATCGCC	ATCAGTGTGC	TCAAGAACCT	GCTGATAAAG	CATTCTTTTG 1440
1441	ATGACAGATA	TGCTTCAAGG	AGCCATCAGG	CAAGGATAGC	CACCCCTTAC	CTGCCCTGT	TTGGTCTGCT	GATTGAAAA 1520
1521	GTCCAGCGGA	TCAATGTGAG	GGATGTGTCA	CCCTTCCCTG	TGAACGCGGG	CATGACCCGT	AAGGATGAAT	CCCTGGCTCT 1600
1601	ACCAGCTGTG	AATCCGCTGG	TGACGCGCGA	GAAGGGAAGC	ACCTGTGGAC	ACAGCCTGCA	CAAGGACCTG	CTGGCGCCCA 1680
1681	TCTCCGCGAT	TGCTTCTCCA	TATACAACCT	CAACTCCAAA	CATCAACAGT	GTGAGAAATG	CTGATTCGAG	AGGATCTCTC 1760
1761	ATAAGCACAG	ATTCGGGTAA	CAGCCTTCCA	GAAGGAATA	GTGAGAAGAG	CAATTCCCTG	GATAAGCACC	AACAAGTAG 1840
1841	CTATTGGGGA	AATTCCTGGG	TTGCTGTGTA	TAACTTGAC	CAGTCTGAGA	TTAAGAGCCT	ACTGATGTGT	TTCTCTTACA 1920
1921	TCTTAAAGAG	CATGCTGTAT	GATGCTTTGT	TTACATATTG	GAACAAGGCT	TCAACATCTG	AACCTTATGA	TTTTTTTACA 2000
2001	ATATCTGAAG	TCTGCCTGCA	CCAGTTCAG	TACATGGGGA	AGCGATACAT	AGCCAGGAAC	CAGGAGGGGT	TGGGACCAT 2080
2081	AGTTCAATGAT	CGAAAGTCTC	AGACATTGCC	TGTTTCCCGT	AACAAGACAG	GAATGATGCA	TGCCAGATTG	CAGCAGCTGG 2160
2161	GCAGCCTGGA	TAACTCTCTC	ACTTTTAACC	ACAGCTATGG	CCACTCGGAC	GCAGATGTTT	TGCACCAAGT	ATTACTTGAA 2240
2241	GCCAACATTG	CTACTGAGGT	TTGCCTGACA	GCTCTGGACA	CGCTTCTCT	ATTTACATTG	CGCTTTAAGA	ACCAGCTCCT 2320
2321	GGCCGACCAT	GGACATAATC	CTCTCATGAA	AAAAGTTTTT	GATGTCTACC	TGTGTTTTCT	TCAAAAACAT	CAGCTGAAAA 2400
2401	CGGCTTTTAA	AAATGTCTTC	ACTGCCTTAA	GGTCCCTTAAT	TATATAAGTT	CCCTCAACAT	TCTATGAAGG	GAGAGCGGAC 2480
2481	ATGTGTGCGG	CTCTGTGTTA	CGAGATTCTC	AAGTGTGTGA	ACTCCAAGCT	GAGCTCCATC	AGGACGGAGG	CCTCCAGCT 2560
2561	CTCTACTTTC	CTGATGAGGA	ACAACTTTGA	TTAACTTGGA	AAGAAGTCCT	TTGTCCGGAC	ACATTTGCAA	GTCTCATAT 2640
2641	GCTGTAGGCA	GCTGATAGCA	GACGTTGTTG	GCATTGGGGA	AACCAGATTC	CAGCAGTCCC	TGTCCATCAT	CAACAACGT 2720
2721	GCCAACAGTG	ACCGGCTTAT	TAAGCACACC	AGCTTCTCCT	CTGATGTGAA	GGACTTAACC	AAAAGGATAC	GCACGGTGCT 2800
2801	AATGGCCACC	GCCCAGATGA	AGGAGCATGA	GAACGACCCA	GAGATGCTGG	TGGACCTCCA	GTACAGCCTG	GCCAAATCCT 2880
2881	ATGCCAGCAC	GCCCAGGCTC	AGGAAGACGT	GGCTCGACAG	CATGGCCAGG	ATCCATGTCA	AAAATGGCGA	TCTCTCAGAG 2960
2961	GCAGCAATGT	GCTATGTCCA	CGTAACAGCC	CTAGTGGCAG	AAATCTCTAC	ACGGAAGGCC	GTGTTTAGAG	AAGGATGCAC 3040
3041	CGCCTTCAGG	GTCAATTACC	CAAAACATCGA	CGAGGAGGCC	TCCATGATGG	AAGACGTGGG	GATGCAGGAT	GTCCATTTC 3120
3121	ACGAGGATGT	GCTGATGGAG	CTCCTTGAGC	AGTGCGCAGA	TGGACTCTGG	AAAGCCGAGC	GCTACGAGCT	CATCGCCGAC 3200
3201	ATCTACAAAC	TTATCATCCC	CATTTATGAG	AAGCGGAGGG	ATTTCTTTGA	AGATGAAGAT	GGAAAGGAGT	ATATTTACAA 3280
3281	GGAAACCCAA	CTCACACCGC	TGTCGGAAAT	TTCTCAGAGA	CTCCTTAAAC	TGTACTCGGA	TAAATTTGGT	TCTGAAAATG 3360
3361	TCAAAATGAT	ACAGGATTCT	GGCAAGGTCA	ACCCTAAGGA	TCTGGATTCT	AAGTATGCAT	ACATCCAGGT	GACTCAGCTC 3440
3441	ATCCCTTCT	TTGACGAAAA	AGAGTTGCAA	GAAGGAATAA	CAGAGTTTGA	GAGATCCAC	AACATCCGCC	GCTTCATGTT 3520
3521	TGAGATGCCA	TTTACGCAGA	CCGGGAAGAG	GCAGGGCGGG	GTGGAAGAGC	AGTGCAAACG	GCGCACCATC	CTGACAGCCA 3600
3601	TACACTGCTT	CCCTTATGTG	AAGAAGCGCA	TCCCTGTAT	GTACCAGCAC	CACACTGACC	TGAACCCCAT	CGAGGTGGCC 3680
3681	ATTGACGAGA	TGAGTAAGAA	GGTGGCGGAG	CTCCGGCAGC	TGTGCTCCTC	GGCCGAGGTG	GACATGATCA	AACTGCAGCT 3760
3761	CAAATCCAG	GGCAGCGTGA	GTGTTCAGGT	CAATGCTGGC	CCACTAGCAT	ATGCGCGAGC	TTTCTTAGAT	GATACAAACA 3840
3841	CAAAGCGGTA	TCCTGACAA	AAAGTGAAGC	TGCTTAAGGA	AGTTTTTCAG	CAATTTGTGG	AAGCTTGGCG	TCAAGCCTTA 3920
3921	CGGGTAAACG	AACGCTGTAT	TAAAGAAGAC	CAGCTCGAGT	ATCAGGAAGA	AATGAAAGCC	AACACAGGG	AAATGGCGAA 4000
4001	GGAGCTTTCT	GAAATCATGC	ATGAGCAGAT	CTGCCCTCTG	GAGGAGAAGA	CGAGCGTCTT	ACCGAATTC	CTTCACATCT 4080
4081	TCAAACGCCAT	CAGTGGGACT	CCAACAAGCA	CAATGGTTCA	CGGGATGACC	AGCTCGTCTT	CGGTCTGTGT	ATTACATCTC 4160
4161	ATGGCCCGTG	TGTGGGGACT	TGCTTTGTCA	TTTGCAAACT	CAGGATGCTT	TCCAAAGCCA	ATCACTGGGG	AGACCGAGCA 4240
4241	CAGGGAGGAC	CAAGGGGAAG	GGGAGAGAAA	GGAAATAAAG	AACAACGTTA	TTTCTTAAAC	GACTTTCTAT	AGGACTTGTA 4320
4321	AGAAGGTGCA	CATATTTTTT	TAAATCTCAC	TGGCAATATT	CAAAGTTTTT	ATTGTGCTCT	AACAAAGGTG	TGGTAGACAC 4400
4401	TCTTGAGCTG	GACTTAGATT	TTATTCTTCC	TTGCAGAGTA	GTGTTAGAA	AGATGGCCTA	CAGAAAAAAA	AGGTTCTGGG 4480
4481	ATCTACATGG	CAGGGAGGGC	TGCACTGACA	TTGATGCGCT	GGGGACCTTT	TGCGCTCGACT	CGTGCCGGAA	ATCTGATCGT 4560
4561	AATCAGGGTA	CAGAACCTAC	TAGTTTGTCT	TAGGAGTATG	TTGTATGACT	AGGATTGTGT	CTATTATCTC	ATTCAACAAC 4640
4641	ATAGAGCAAG	AATAGTGAGC	TAACTGAGCT	AGACACTCAA	TTAATCCGCT	ACTGGCTTGG	AGTCAGAACT	TTGTCATTAA 4720
4721	TCATCGACTC	CGGGACGGTC	ATATATGTAT	TACATTTCTA	CATTTTAAAT	ACTCACATGG	GCTTATGCAT	TAAAGTTAAT 4800
4801	TGTATAAAT	TTGTGCTGGT	CCAGTATATG	CAATACACTT	TAATGGTTTA	TTCTTGTCT	AAAAATGTGC	AATATGGAGA 4880
4881	TGTATACAAG	TCTTTACT						4898
	10	20	30	40	50	60	70	80

FIG.10C

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	10	20	30	40	50	60	70	80	
1	MEGHVMI	PTILNQLFRV	LTRATQEEVA	VNVTRVHHV	VAQCHEEGLE	SHLRSYVKYA	YKAEPYVASE	YKTVHEELTK	80
81	SMTTILKPSA	DFLTSNKLLR	YSWFFFDVLI	KSMAQH LIEN	SKVKLLRNQR	FPASYHHAEE	TVVNMLMPHI	TQKFGDNPEA	160
161	SKNANHSLAV	FIKRCFTFMD	RGFVFKQINN	YISCFAPGDP	KTLEFYKFEF	LRVVCNHEHY	IPLNLPMPFG	KGRIQRYQDL	240
241	QLDYSLTDEF	CRNHFLVGLL	LREVGTA LQE	FREVRLIAIS	VLKNLLIKHS	FDDRYASRSH	QARIATLYLP	LFGLLIENVQ	320
321	RINVRDVSPF	PVNAGMTVKD	ESLALPAVNP	LVT PQKGSTL	DNSLHKDLLG	AISG IASPYT	TSTPNINSVR	NADSRGSLIS	400
401	TDSGNSLPER	NSEKSNSLDK	HQSSSTLGNS	VVRCDKLDQS	EIKSLIMCFL	YILKSMSDDA	LFTYWNKAST	SEIMDFFTIS	480
481	EVCLHQFYM	GKRYIARNQE	GLGP IVHDRK	SQTLFVSRRR	TGMMHARLQQ	LGSLDNLSTF	NHSYGHSDAD	VLHQSLLEAN	560
561	IATEVCLTAL	DTLSLFTLAF	KNQLLADHGH	NPLMKKVFDV	YLCFLQKHQS	ETALKNVFTA	LRS LIYKFPS	TFYEGRADMC	640
641	AALCYEILKC	CNSKLS SIRT	EASQLLYFLM	RNNFDYTGKK	SFVRTHLQVI	ISVSQ LIADV	VGIGETR FQQ	SLSIINN CAN	720
721	SDRLIKHTSF	SSDVKOLTKR	IRTVLMATAQ	MKEHENDPEM	LVDLQYSLAK	SYASTPELRK	TWLD SMARIH	VKNGDLSEAA	800
801	MCYVHV TALV	AEYLTRKGVF	RQCCTAFRVI	TPNIDEEASM	MEDVGMQDVH	FNEDVLMELL	EQCADGLWKA	ERYELIADIY	880
881	KLIPIYIEKR	RDFFEDEDGK	EYIYKEPKLT	PLSEISQRLL	KLYSDKFGSE	NVKMIQDSGK	VNPKDLD SKY	AYIQVTHVIP	960
961	FFDEKELQER	KTEFERSHNI	RREFMFEMFFT	QTGKRQGGVE	EQCKRRTILT	AIHCFFPYVKK	RIPVMYQHHT	DLNPIEVAID	1040
1041	EMSKKVAELR	QLCSSAEVDM	IKLQLKLQGS	VSVQVNAGPL	AYARAF LDDT	NTKRYPDNKV	KLLKEVFRQF	VEACGQALAV	1120
1121	NERLIKEDQL	EYQEEMKANY	REMAKELSEI	MHEQICPLEE	KTSVLPNSLH	IFNAISGTPT	STMVHGMTSS	SSVV	1195

FIG. 10C (cont.)

	10	20	30	40	50	60	70	80	
1	AATTGTAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG	GCCCCCCTC	GAGGTCGACG	GTATCGATAA	GCTTGATATC	80
81	GAATTCGGCA	CGAGTTTATC	ACCATCACCA	AAACCCAGAA	TTTTATGATG	AGATTAAAT	AGAGTTGCC	ACTCAGCTGC	160
161	ATGAAAAGCA	CCACCTGTTG	CTCACATTCT	TCCATGTCA	CTGTGACAC	TCAAGTAAAG	GAAGCAGGAA	GAAGAGGGAT	240
241	GTGTTGAAA	CCCAAGTTGG	CTACTCCTGG	CTTCCCCTCC	TGAAAGACGG	AAGGGTGGTG	ACAAGCGAGC	AGCACATCCC	320
321	GGTCTCGGCG	AACCTTCCTT	CGGGCTATCT	TGGCTACCAA	GAGCTTGGGA	TGGGCAGGCA	TTATGGTCCG	GAATTTAAAT	400
401	GGGTAGATGG	AGGCAAGCCA	CTGCTGAAAA	TTTCCACTCA	TCTGGTTTCT	ACAGGGATAC	TCAGGATCAG	CATTTACATA	480
481	ATTTTTTCCA	GTACTGTCTG	AAAACCGAAT	CTGGAGCCCA	AGCCTTAGGA	AACGAACCTG	TAAAGTACCT	TAAGAGTCTG	560
561	CATGCGATGG	AAGGCCACGT	GATGATCGCC	TTCTTGCCCA	CTATCCTAAA	CCAGCTGTTC	CGAGTCTCTA	CCAGAGCCAC	640
641	ACAGGAAGAA	GTCCGCGTTA	ACGTGACTCG	GCTCATTTAT	CATGTGGTTG	CCCAGTGCCA	TGAGGAAGGA	TTGGAGAGCC	720
721	ACTTGAGGTC	ATATGTTAAG	TACGCGTATA	AGGCTGAGCC	ATATGTTGCC	TCTGAATACA	AGACAGTGCA	TGAAGAAGCTG	800
801	ACCAAAATCCA	TGACCACGAT	TCTCAAGCCT	TCTGCCGATT	TCTCACCCAG	CAACAACTA	CTGAGGTACT	CATGGTTTTT	880
881	CTTTGATGTA	CTGATCAAAAT	CTATGGCTCA	GCATTTGATA	GAGAATCCCA	AAGTTAAGTT	GCTGCCGAAC	CAGAGATTTT	960
961	CTGCATCCTA	TCATCATGCA	GCGGAAACCG	TTGTAAATAT	GCTGATGCCA	CACATCACTC	AGAAGTTTGG	AGATAATCCA	1040
1041	GAGGCACTTA	AGAACGCGAA	TCATAGCCTT	GCTGTCTTCA	TCAGAGATG	TTTCCACCTT	ATGGACAGGG	GCTTTGTCTT	1120
1121	CAAGCAGATC	AACAACCTACA	TTAGCTGTTT	TGCTCCTGGA	GACCCAAAGA	CCCTCTTTGA	ATACAAGTTT	GAATTTCTCC	1200
1201	GTGTAGTGTG	CAACCATGAA	CATTATATTC	CGTTGAACCT	ACCAATGCCA	TTTGGAAAG	GCAGGATTC	AGATATCCAA	1280
1281	GACCTCCAGC	TTGACTACTC	ATTAACAGAT	GAGTTCTGCA	GAAACCACTT	CTTGGTGGGA	CTGTTACTGA	GGGAGGTGGG	1360
1361	GACAGCCCTC	CAGGAGTTCC	GGGAGGTCCG	TCTGATCGCC	ATCAGTGTGC	TCAAGAACCT	GCTGATAAAG	CATTTCTTTG	1440
1441	ATGACAGATA	TGCTTCAAGG	AGCCATCAGG	CAAGGATAGC	CACCTCTAC	CTGCCCTGTG	TTGGTCTGCT	GATTGAAAAC	1520
1521	GTCAGCGGGA	TCAATGTGAG	GGATGTGTCA	CCCTTCCCTG	TGAACGCGGG	CATGACCGTG	AAGGATGAAT	CCCTGGCTCT	1600
1601	ACCAGCTGTG	AATCCGCTGG	TGACGCGCGA	GAAGGGAAGC	ACCCTGGACA	ACAGCCTGCA	CAAGGACCTG	CTGGGCGCCA	1680
1681	TCTCCGGCAT	TGCTTCTCCA	TATACAACCT	CAACTCCAAA	CATCAACAGT	GTGAGAAATG	CTGATTCGAG	AGGATCTCTC	1760
1761	ATAAGCACAG	ATTCGGGTAA	CAGCCTTCCA	GAAAGGAATA	GTGAGAAAG	CAATTCCTTG	GATAAGCACC	AACAAAGTAG	1840
1841	CACATTGGGA	AATTCGCTGG	TTGCTGTGTA	TAACTTGAC	CAGTCTGAGA	TTAAGAGCCT	ACTGATGTGT	TTCTCTTACA	1920
1921	TCTTAAAGAG	CATGCTGTAT	GATGCTTTGT	TTACATATTG	GAACAAGGCT	TCAACATCTG	AACCTTATGA	TTTTTTTACA	2000
2001	ATATCTGAAG	TCTGCCCTGCA	CCAGTTCCAG	TACATGGGGA	AGCCATACAT	AGCCAGGAAC	CAGGAGGGGT	TGGGACCCAT	2080
2081	AGTTTCATGAT	CGAAAGTCTC	AGACATTGCC	TGTTTCCCGT	AACAGAACAG	GAATGATGCA	TGCCAGATTG	CAGCAGCTGG	2160
2161	GCAGCCTGGA	TAACTCTCTC	ACTTTTAAAC	ACAGCTATGG	CCACTCGGAC	GCAGATGTTT	TGCACCATG	ATTACTTGAA	2240
2241	GCCAAACATT	CTACTGAGGT	TTGCTGTACA	GCTCTGGACA	CGTCTCTCT	ATTTTACATT	GCGTTTAAAG	ACCAGCTCCT	2320
2321	GGCCGACCAT	GGACATAATC	CTCTCATGAA	AAAAGTTTTT	GATGTCTTACC	TGTGTTTTCT	TCAAAAACAT	CAGTCTGAAA	2400
2401	CGGCTTTAAA	AAATGTCTTC	ACTGCCCTTAA	GGTCCCTTAA	TTATAAGTTT	CCCTCAACAT	TCATGAAGG	GAGAGCGGAC	2480
2481	ATGTTGTGCG	CTCTGTGTTA	CGAGATTCTC	AAGTGCTGTA	ACTCCAAGCT	GAGCTCCATC	AGGACGGAGG	CCTCCAGGCT	2560
2561	GCTCTACTTC	CTGATGAGGA	ACAACCTTGA	TTACACTGGA	TTATCTTCTC	TGTCCTATCA	CAACAACCTG	TCTCTCAGAG	2640
2641	CTGTACGCCA	GCTGATAGCA	GACGTGTGTT	GCATTGGGGG	AAGAACTCCT	TGTCCTGCGG	ACATTTGCAA	GTCATCATAT	2720
2721	GCCAAACAGT	ACCGGCTTAT	TAAGCACACC	AGCTTCTCCT	CTGATGTGAA	GGACTTAACC	AAAAGGATAC	GCACGGTGCT	2800
2801	AATGGCCACC	GCCCAGATGA	AGGAGCATGA	GAACGACCCA	GAGATGCTGG	TGGACCTCCA	GTACAGCCTG	GCCAAATCCT	2880
2881	ATGCCAGCAC	GCCCGAGCTC	AGGAAGACGT	GGCTGCACAG	CATGGCCAGG	ATCCATGTCA	AAAATGGCCA	GAGAGCGGAC	2960
2961	GCAGCAATGT	GCTATGTCCA	CGTAACAGCC	CTAGTGGCAG	AAATCTCTAC	ACGGAAAGGC	GTGTTTAGAC	AAGGATGCAC	3040
3041	CGCCTTCAGG	GTCATTACCC	CAAAACATCGA	CGAGGAGGCC	TCCATGATGG	AAGACGTGGG	GATGCAGGAT	GTCCATTCCA	3120
3121	ACGAGGATGT	GCTGATGGAG	CTCCTTGAGC	AGTGGCGAGA	TGGACTCTGG	AAAGCCGAGC	GCTACGAGCT	CATCGCGCAC	3200
3201	ATCTACAAAC	TTATCATCCC	CATTTATGAG	AAGCGGAGGG	ATTTCTTTGA	AGATGAAGAT	GGAAGGAGT	ATATTTACAA	3280
3281	GGAAACCCAAA	CTCACACCCG	TGTCGGAAAT	TTCTCAGAGA	CTCCTTAAAC	TGTACTCGGA	TAAATTTGGT	TCTGAAAATG	3360
3361	TCAAATATGAT	ACAGGATTCT	GGCAAGGTCA	ACCCTAAGGA	TCTGGATTCT	AAGTATGCAT	ACATCCAGGT	GACTCAGCTC	3440
3441	ATCCCTTTCT	TTGACGAAAA	AGAGTTGCAA	GAAAGGAAAA	CAGAGTTTGA	GAGATCCAC	AACATCCGCC	GCTTCATGTT	3520
3521	TGAGATGCCA	TTTACGCAGA	CCGGGAAGAG	GCAGGGCGGG	GTGGAAGAGC	AGTGCAACGC	GCGCACCATC	CTGACAGCCA	3600
3601	TACACTGCTT	CCCTTATGTG	AAGAAGCGCA	TCCTTGTCAT	GTACCAGCAC	CACACTGACC	TGAACCCCAT	CGAGGTGGCC	3680
3681	ATTGACGAGA	TGAGTAAGAA	GGTGGCGGAG	CTCCGGCAGC	TGTGCTCCTC	GGCCGAGGTG	GACATGATCA	AACTGCAGCT	3760
3761	CAAACTCCAG	GGCAGCGTGA	GTGTTCAAGT	CAATGCTGGC	CCACTAGCAT	ATGCGCGAGC	TTTCTTAGAT	GATACAAACA	3840
3841	CAAAGCGATA	TCCTGACAAT	AAAGTGAAGC	TGCTTAAAGGA	AGTTTTTCAG	CAATTTGTGG	AAGCTTGCGG	TCAAGCCTTA	3920
3921	GCGGTAACAG	AACGTCTGAT	TAAAGAAGAC	CAGCTCGAGT	ATCAGGAAGA	AATGAAAGCC	AACTACAGGG	AAATGGCGAA	4000
4001	GGAGCTTTCT	GAAATCATGC	ATGAGCAGAT	CTGCCCTCTG	GAGGAGAAGA	CGAGCGTCTT	ACCGAATTC	CTTCACATCT	4080
4081	TCAACGCCAT	CAGTGGGACT	CCAACAAGCA	CAATGGTTCA	CGGGATGACC	AGCTCGTCTT	CGGTGCTGTG	ATTACATCTC	4160
4161	ATGGCCCGTG	TGTGGGGACT	TGCTTTGTCA	TTTTCGAACT	CAGGATGCTT	TCCAAAGCCA	ATCACTGGGG	AGACCGAGCA	4240
4241	CAGGGAGGAC	CAAGGGGAAG	GGGAGAGAAA	GGAATAAAG	AACAACGTTA	TTTCTTAAAC	GACTTTCTAT	AGGAGTTGTA	4320
4321	AGAAGGTGCA	CATATTTTTT	TAAATCTCAC	TGGCAATATT	CAAAGTTTTC	ATTGTGTCTT	AACAAAGGTG	ATTCAACAC	4400
4401	TCTTGAGCTG	GACTTAGATT	TTATTTCTCC	TTGCAGAGTA	GTGTTAGAAAT	AGATGGCCTA	CAGAAAAAAG	AGGTTCTGGG	4480
4481	AATCTACATGG	CAGGGAGGGC	TGCACTGACA	TTGATGCTGT	GGGGACCTTT	TGCTCGACT	CGTGCCGGAA	ATCTGATCGT	4560
4561	AATCAGGGTA	CAGAACTTAC	TAGTTTTGTC	TAGGAGTATG	TTGTATGACT	AGGATTTGTG	CTATTATCTC	ATTCAACAC	4640
4641	ATAGAGCAAG	AATAGTGAGC	TAACTGAGCT	AGACACTCAA	TTAATCCGCT	ACTGGCTTCA	AGTCAGAACT	TTGTCATTAA	4720
4721	TCATCGACTC	CGGGACGGTC	ATATATGTAT	TACATTTCTA	CATTTTTTAA	ACTCACATGG	GCTTATGCAT	TAAGTTTAAAT	4800
4801	TGTGATAAAT	TTGTGCTGGT	CCAGTATATG	CAATACACTT	TAATGGTTTA	TTCTGTGCAT	AAAAATGTGC	AATATGGAGA	4880
4881	TGTATACAAG	TCCTTACT							4898

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		10		20		30		40		50		60		70		80																																																																	
1	MEGHV	MI	AF	PTILN	QL	FRV	L	TRATQ	EE	V	VNV	TRV	I	H	V	VAQC	CHEE	G	LE	SHL	RSY	V	K	Y	A	Y	K	A	E	P	V	V	A	S	E	Y	K	T	V	H	E	E	L	T	K	80																																			
81	SMT	TIL	K	P	S	A	D	E	L	T	S	N	K	L	L	R	Y	S	W	F	F	F	D	V	L	I	K	S	M	A	O	H	L	I	E	N	S	K	V	K	L	L	R	N	Q	R	160																																		
161	SKN	AN	H	S	L	A	V	F	I	K	R	C	F	T	F	M	D	R	G	F	V	F	K	Q	I	N	N	Y	I	S	C	F	A	P	G	D	P	K	T	L	F	E	Y	K	F	E	F	L	R	V	C	N	H	E	H	Y	I	P	L	N	L	P	M	P	F	G	K	G	R	I	Q	R	Y	Q	D	L	240				
241	QLD	Y	S	L	T	D	E	F	C	R	N	H	F	L	V	G	L	L	L	R	E	V	G	T	A	L	Q	E	F	R	E	V	R	L	I	A	I	S	V	L	K	N	L	L	I	K	H	S	F	D	D	R	Y	A	S	R	S	H	Q	A	R	I	A	T	L	Y	L	P	L	F	G	L	L	I	E	N	V	Q	320		
321	RIN	V	R	D	V	S	P	E	F	V	N	A	G	M	T	V	K	D	E	S	L	A	L	P	A	V	N	P	L	V	T	P	Q	K	G	S	T	L	D	N	S	L	H	K	D	L	L	G	A	I	S	G	I	A	S	P	Y	T	T	S	T	P	N	I	N	S	V	R	N	A	D	S	R	G	S	L	I	S	400		
401	TDS	G	N	S	L	P	E	R	N	S	E	K	S	N	S	L	D	K	H	Q	Q	S	S	T	L	G	N	S	V	V	R	C	D	K	L	D	Q	S	T	G	M	M	H	A	R	L	Q	Q	L	G	S	L	D	N	S	L	T	F	N	H	S	Y	G	H	S	D	A	D	V	L	H	Q	S	L	L	E	A	N	560		
481	EV	C	L	H	Q	F	Q	Y	M	G	K	R	Y	I	A	R	N	Q	E	G	L	G	P	I	V	H	D	R	K	S	Q	T	L	F	V	S	R	N	R	T	G	M	M	H	A	R	L	Q	Q	L	G	S	L	D	N	S	L	T	F	N	H	S	Y	G	H	S	D	A	D	V	L	H	Q	S	L	L	E	A	N	640	
561	I	A	T	E	V	C	L	T	A	L	D	T	L	S	L	F	T	L	A	F	K	N	Q	L	L	A	D	H	G	H	N	P	L	M	K	K	V	E	D	V	Y	L	C	F	L	Q	K	H	Q	S	E	T	A	L	K	N	V	F	T	A	L	R	S	L	I	Y	K	F	P	S	T	F	Y	E	G	R	A	D	M	C	640
641	A	A	L	C	Y	E	I	L	K	C	C	N	S	K	L	S	S	I	R	T	E	A	S	Q	L	L	Y	F	L	M	R	N	N	E	D	Y	T	G	K	K	L	V	D	L	Q	Y	S	L	A	K	S	Y	A	S	T	P	E	L	R	K	T	W	L	D	S	M	A	R	I	H	V	K	N	G	D	L	S	E	A	A	800
721	S	D	R	L	I	K	H	T	S	F	S	S	D	V	K	D	L	T	K	R	I	R	T	V	L	M	A	T	A	Q	M	K	E	H	E	N	D	P	E	M	L	V	D	L	Q	Y	S	L	A	K	S	Y	A	S	T	P	E	L	R	K	T	W	L	D	S	M	A	R	I	H	V	K	N	G	D	L	S	E	A	A	800
801	M	C	Y	V	H	V	T	A	L	V	A	E	Y	L	T	R	K	G	V	E	R	Q	G	T	A	F	R	V	I	T	P	N	I	D	E	E	A	S	M	M	E	D	V	M	G	M	Q	D	V	H	F	N	E	D	V	L	M	E	L	L	E	Q	C	A	D	G	L	W	K	A	E	R	Y	E	L	I	A	D	I	Y	880
881	K	L	I	P	I	Y	E	K	R	R	D	F	F	E	D	E	D	G	K	E	Y	I	Y	K	E	P	K	L	T	P	L	S	E	I	S	Q	R	L	L	K	L	Y	S	D	K	F	G	S	E	N	V	K	M	I	Q	D	S	G	K	V	N	P	K	D	L	S	K	Y	A	Y	I	Q	V	T	H	V	I	P	960		
961	F	F	D	E	K	E	L	Q	E	R	K	T	E	F	E	R	S	H	N	I	R	R	F	M	F	E	M	P	F	T	Q	T	G	K	R	Q	G	G	V	E	E	Q	C	K	R	R	T	I	L	T	A	I	H	C	F	P	Y	V	K	K	R	I	P	V	M	Y	Q	H	H	T	D	L	N	P	I	E	V	A	I	D	1040
1041	E	M	S	K	K	V	A	E	L	R	Q	L	C	S	S	A	E	V	D	M	I	K	L	Q	L	K	L	Q	G	S	V	S	V	Q	V	N	A	G	P	L	A	Y	A	R	A	F	L	D	D	T	N	T	K	R	Y	P	D	N	K	V	K	L	L	K	E	V	F	R	Q	F	V	E	A	C	G	Q	A	L	A	V	1120
1121	N	E	R	L	I	K	E	D	Q	L	E	Y	Q	E	E	M	K	A	N	Y	R	E	M	A	K	E	L	S	E	I	M	H	E	Q	I	C	P	L	E	E	K	T	S	V	L	E	N	S	L	H	I	F	N	A	I	S	G	T	P	T	S	T	M	V	H	G	M	T	S	S	S	V	1195								
		10		20		30		40		50		60		70		80																																																																	

FIG. 10D(cont.)

	10	20	30	40	50	60	70	80	
1	AATTGTAATA	CGACTCACTA	TAGGCGCAAT	TGGGTACCGG	CCCCCCCCCTC	GAGGTCGACG	GTATCGATAA	GCTTGATATC	80
81	GAATTCGGCA	CGAGTTTAC	ACCATCACCA	AAACCCAGAA	TTTTATGATG	AGATTAAAAAT	AGAGTTGCCC	ACTCAGCTGC	160
161	ATGAAAAGCA	CCACCTGTTG	CTCACATTCT	TCCATGTCTAG	CTGTGACAAC	TCAAGTAAAG	GAAGCAGGAA	GAAGAGGGAT	240
241	GTCGTTGAAA	CCCAAGTTGG	CTACTCCTGG	CTTCCCCCTCC	TGAAAGACGG	AAGGGTGGTG	ACAAGCGAGC	AGCACATCCC	320
321	GGTCTCGGCG	AACCTTCCTT	CGGGCTATCT	TGGCTACCAA	GAGCTTGGGA	TGGGCAGGCA	TTATGGTCCG	GAAATTAAT	400
401	GGGTAGATGG	AGGCAAGCCA	CTGCTGAAAA	TTTCCACTCA	TCTGGTTTCT	ACAGGGATAC	TCAGGATCAG	CATTTACATA	480
481	ATTTTTTCCA	GTACTGTGAG	AAAACCGAAT	CTGGAGCCCA	AGCCTTAGGA	AACGAACCTG	TAAAGTACCT	TAAGAGTCTG	560
561	CATGCGATGG	AAGGCCACGT	GATGATCGCC	TTCTTGCCCA	CTATCCTAAA	CCAGCTGTTC	CGAGTCTCTA	CCAGAGCCAC	640
641	ACAGGAAGAA	GTCCGCGTTA	ACGTGACTCG	GGTCATTATT	CATGTGGTTG	CCCAGTGCCA	TGAGGAAGGA	TTGGAGAGCC	720
721	ACTTGAGGTC	ATATGTTAAG	TACGCGTATA	AGGCTGAGCC	ATATGTTGCC	TCTGAATACA	AGACAGTGCA	TGAAGAACTG	800
801	ACCAATATCCA	TGACCACGAT	TCTCAAGCCT	TCTGCCGATT	TCCTCACCAG	CAACAAACTA	CTGAGGTACT	CATGGTTTTT	880
881	CTTTGATGTA	CTGATCAAAAT	CTATGGCTCA	GCATTTGATA	GAGAACTCCA	AAGTTAAGTT	GCTGCGAAAC	CAGAGATTTT	960
961	CTGCATCCTA	TCATCATGCA	GCGGAAACCG	TTGTAAATAT	GCTGATGCCA	CACATCACTC	AGAAGTTTGG	AGATAATCCA	1040
1041	GAGGCATCTA	AGAACGCGAA	TCATAGCCTT	GCTGTCTTCA	TCAAGAGATG	TTTCACCTTC	ATGGACAGGG	GCCTTGTCTT	1120
1121	CAAGCAGATC	AACAACATACA	TTAGCTGTTT	TGCTCCTGGA	GACCCAAAGA	CCCTCTTTGA	ATACAAGTTT	GAATTTCTCC	1200
1201	GTGTAGTGTG	CAACCATGAA	CATTATATTC	CGTTGAACCT	ACCAATGCCA	TTTGGAAAAG	GCAGGATTCA	AGATACCAA	1280
1281	GACCTCCAGC	TTGACTACTC	ATTAACAGAT	GAGTTCTGCA	GAAACCACTT	CTTGGTGGGA	CTGTTACTGA	GGGAGGTGGG	1360
1361	GACAGCCCTC	CAGGAGTTCC	GGGAGGTCCG	TCTGATCGCC	ATCAGTGTGC	TCAAGAACCT	GCTGATAAAG	CATTCTTTTG	1440
1441	ATGACAGATA	TGCTTCAAGG	AGCCATCAGG	CAAGGATAGC	CACCCCTTAC	CTGCCCTCTG	TGGTCTGCT	GATTGAAAAC	1520
1521	GTCCAGCGGA	TCAATGTGAG	GGATGTGTCA	CCCTTCCCTG	TGAACCGCGG	CATGACCGTG	AAGGATGAAT	CCCTGGCTCT	1600
1601	ACCAGCTGTG	AATCCGCTGG	TGACGCCGCA	GAAGGGAAGC	ACCTTGAGCA	ACAGCCTGCA	CAAGGACCTG	CTGGGCGCCA	1680
1681	TCTCCGGCAT	TGCTTCTCCA	TATACAACCT	CAACTCCAAA	CATCAACAGT	GTGAGAAATG	CTGATTCCGAG	AGGATCTCTC	1760
1761	ATAAGCACAG	ATTCGGGTAA	ATTCGCTGG	TTCGCTGTGA	TAAACTTGAC	GAACAAGGCT	TCAACATCTG	AACCTTATGGA	1840
1841	CACATTGGGA	AATTCGCTGG	TTCGCTGTGA	TAAACTTGAC	GAACAAGGCT	TCAACATCTG	AACCTTATGGA	TTTCTTCTCA	1920
1921	TCTTAAAGAG	CATGCTCTGAT	GATGCTTTGT	TTACATATTG	AGCCATACAT	AGCCAGGAAC	CAGGAGGGGT	TGGGACCCAT	2000
2001	ATATCTGAAG	TCTGCCTGCA	CCAGTTCCAG	TACATGGGGA	AACAGAACAG	GAATGATGCA	TGCCAGATTC	CAGCAGCTGG	2080
2081	AGTTTCATGAT	CGAAAGTCTC	AGACATTGCC	TGTTTCCCGT	CCACTCGGAC	GCAGATGTTT	TGCACGATC	ATTACTTGAA	2160
2161	GCAGCCTGGA	TAACTCTCTC	ACTTTTAAAC	ACAGCTATGG	CGCTTTCTCT	ATTTACATTG	CGGTTTAAAG	ACCAGCTCCT	2240
2241	GCCAAACATTG	CTACTGAGGT	TTGCCTGACA	GCTCTGGACA	GATGCTTACC	TGTGTTTCTT	TCAAAAACAT	CAGTCTGAAA	2320
2321	GGCCGACCAT	GGACATAATC	CTCTCATGAA	AAAAGTTTTT	TTATAAGTTT	CCCTCAACAT	CTATGAAGG	GAGAGCGGAG	2400
2401	CGGCTTTTAA	AAATGCTCTC	ACTGCCTTAA	GGTCCTTAAT	ACTTCAAGCT	GAGCTCCATC	AGGACGGAGG	CCTCCAGCT	2480
2481	ATGTGTGCGG	CTCTGTGTTA	CGAGATTCTC	AAGTCTGTGA	AAGAAGTCTT	TTGTCCGGAC	ACATTTGCAA	GTCTCATAT	2560
2561	GCTCTACTTC	CTGATGAGGA	ACAACTTTGA	TTACACTGGA	AACAGATTTC	CAGCAGTCCC	TGTCCATCAT	CAACAACGTG	2640
2641	CTGTCTAGCA	GCTGATAGCA	GACGTTGTTG	GCATTGGGGA	CTGATGTGAA	GGACTTAAAC	AAAAGGATAC	GCACGGTCT	2720
2721	GCCAAACAGTG	ACCGGCTTAT	TAAACACACC	AGCTTCTCCT	GAGATGCTGG	TGGACCTCCA	GTACAGCCTG	GCCAAATCCT	2800
2801	AATGGCCACC	GCCAGATGTA	AGGAGCATGA	GAACGACCCA	CATGGCCAGG	ATCCATGTCA	AAAATGGCGA	TCTCTCAGAG	2880
2881	ATGCCAGCAC	GCCCGAGCTC	AGGAAGACGT	GGCTCGACAG	AAATCTCTAC	ACGGAAAGGC	GTGTTTAGAC	AAGGATGCAC	2960
2961	GCAGCAATGT	GCTATGTCCA	CGTAACAGCC	CTAGTGGCAG	TCCATGATGG	AAGACGTGGG	GATGCAAGAT	GTCCATTCCA	3040
3041	CGCCTTCAGG	GTCATTACCC	CAAAACATCGA	CGAGGAGGCC	TGGACTCTGG	AAAGCCGAGC	GCTACGAGCT	CATCGCCGAC	3120
3121	ACGAGGATGT	GCTGATGGAG	CTCCTTGAGC	AGTGCCGAGA	ATTTCTTTGA	AGATGAAGAT	GGAAAGGAGT	ATATTACAA	3200
3201	ATCTACAAAC	TTATCATCCC	CATTTATGAG	AAGCGGAGGG	CTCCTTAAAC	TGTACTCGGA	TAAATTTGGT	TCTGAAAATG	3280
3281	GGAAACCCAAA	CTCACACCGC	TGTCGGAAAT	TTCTCAGAGA	TCTGGATTCT	AAGTATGCA	TAATTTTGGT	TCTGAAAATG	3360
3361	TCAAAATGAT	ACAGGATTCT	GGCAAGGTCA	ACCTTAAGGA	CAGAGTTTGA	GAGATCCAC	AACATCCGCC	GCTTCATGTT	3440
3441	ATCCCCCTCT	TTGACGAAAA	AGAGTTGCAA	GAAGGAAAAA	GTGGAAGAGC	AGTGCAAAAC	GCGCACCATC	CTGACAGCCA	3520
3521	TGAGATGCCA	TTTACGCGAG	CCGGGAAGAG	GCAGGGCGGG	GTACCAGCAC	CACACTGACC	TGAACCCCAT	CGAGGTGGCC	3600
3601	TACACTGCTT	CCCTTATGTG	AAGAAGCGCA	TCCCTGTCTG	TGTGCTCCTC	GGCCGAGGTG	GACATGATCA	AACCTGCAGT	3680
3681	ATTGACGAGA	TGAGTAAGAA	GGTGCGGAG	CTCCGGCAGC	CCACTAGCAT	ATGCGCGAGC	TTTCTTAGAT	GATACAAACA	3760
3761	CAAACTCCAG	GGCAGCGTGA	GTGTTTCAGG	CAATGCTGGC	AGTTTTCAGG	CAATTTGTGG	AAGCTTGCGG	TCAAGCCTTA	3840
3841	CAAAGCGATA	TCCTGACAA	AAAGTGAAGC	TGCTTAAGGA	ATCAGGAAGA	AATGAAAGCC	AACCTACAGG	AAATGGCGAA	3920
3921	GCGGTAAACG	AACGTCTGAT	TAAAGAAGAC	CAGCTCGAGT	GAGGAGAAGA	CGAGCGTCTT	ACCGAATTC	CTTCACATCT	4000
4001	GGAGCTTTCT	GAAATCATGC	ATGAGCAGAT	CTGCCCCCTG	CGGGATGACC	AGCTCGTCTT	CGGTCTGTG	ATTACATCTC	4080
4081	TCAACGCCAT	CAGTGGGACT	CCAACAAGCA	CAATGGTTCA	GTGTTTGAAT	TCCAAAGCCA	ATCACTGGGG	AGACCGAGCA	4160
4161	ATGGCCCGTG	TGTGGGGACT	TGCTTTGTCA	TTTGCAAACT	AACAACGTTA	TTTCTTAAAC	GACTTTCTAT	AGGAGTTGTA	4240
4241	CAGGGAGGAC	CAAGGGGAAG	GGGAGAGAAA	GGAATAAAG	CAAAGTTTTC	ATTGTGTCTT	AACAAGAGTG	TGGTAGACAC	4320
4321	AGAAAGGTGCA	CATATTTTTT	TAAATCTCAT	TGGCAATATT	GGGGACCTTT	TGCCCTCGACT	CGTGCCGGAA	ATCTGATCGT	4400
4401	TCTTGAGCTG	GACTTAGATT	TTATTTCTCC	TGTCAGAGTA	TTGTATGACT	AGGATTGTG	CTATTATCTC	TAATCAACAC	4480
4481	ATCTACATGG	CAGGGAGGGC	TGCACTGACA	TTGATGCCTG	TTAATCCGCT	ACTGGCTTCA	AGTCAGAACT	TTGTCAATTA	4560
4561	AATCAGGGTA	CAGAACTTAC	TAGTTTGTG	TAGGAGTATG	CATTTTAAAT	ACTCACATGG	GCTTATGCAT	TAAGTTTAAAT	4640
4641	ATAGAGCAAG	AATAGTGAGC	TAACTGAGCT	AGACACTCAA	TAATGTTTAA	TTCTTGTCAT	AAAAATGTGC	AATATGGAGA	4720
4721	TCATCGACTC	CGGGACGGTC	ATATATGTAT	TACATTTCTA	TAATGTTTAA	TTCTTGTCAT	AAAAATGTGC	AATATGGAGA	4800
4801	TGTGATAAAT	TTGTGCTGGT	CCAGTATATG	CAATCAACTT	TAATGTTTAA	TTCTTGTCAT	AAAAATGTGC	AATATGGAGA	4880
4881	TGTATACAAG	TCCTTACT							4898

FIG.10E

	10	20	30	40	50	60	70	80							
1	MEGHVMI	PTILNQL	FRV	LTRATQEE	VA	VAQCHEEGLE	SHLRSYV	KYA	YKAEPIVASE	YKTVHEELTK	80				
81	SMTTILK	PSA	DELT	SNKLLR	YSWFFFD	VLI	KSMAQH	LIE	TVVNMLMPHI	TQKFGDNPEA	160				
161	SKNANH	SLAV	FIKRCFT	FMD	RGFVFKQ	INN	YISCFAP	GDP	KTLFEYKFEF	LRVVCNHEHY	IPLNLPMPFG	KGRIQRYQDL	240		
241	QLDYS	LTDEF	CRNHFL	VGLL	LREVG	TALQE	FREVRL	IAIS	VLKNLLIKHS	FDDRYASRSH	QARIATLYLP	LFGLLIENVQ	320		
321	RINVRD	VSPF	FVNAGMT	VKD	ESLAL	PAVNP	LVTPQK	GSTL	DNSLHKDLLG	AISGIASPYT	TSTPNINSVR	NADSRGSLIS	400		
401	TDSGNS	LPER	NSEKNS	SLDK	HQOSS	TLGNS	VVRCD	KLDQS	EIKSLLMCFL	YILKSMSDDA	LFTYWNKAST	SELMDFFTIS	480		
481	EVCLHQ	FQYM	GKRYIAR	NQE	GLGPI	VHDK	SQTLFV	SRNR	TGMMHARLQQ	LGSLDNSLTF	NHSYGHSDAD	VLHQSLLEAN	560		
561	IATEVCL	TAL	DTLSL	FTLAF	KNQLL	ADHGH	NPLMKK	VFDV	YLCFLQKHQS	ETALKNVFTA	LRSLIYKFPS	TFYEGRADMC	640		
641	AALCYE	ILKC	CNSKL	SSIRT	EASQL	LYFLM	RNNFDY	TGKK	SEVVRTHLQVI	ISVSQLIADV	VGIGETRFQQ	SLSIINNCAN	720		
721	SDRLIK	HTSF	SSDVK	DLTKR	IRTVL	MATAQ	MKEHEND	PEM	LVDLQYSLAK	SYASTPELRK	TWLDSMARIH	VKNGDLSEAA	800		
801	MCYVHV	TALV	AEYLTR	KGVF	RQGCTA	FRVI	TPNIDEE	EASM	MEDVGMQDVH	FNEDVLMELL	EQCADGLWKA	ERYELIADIY	880		
881	KLIPIY	EKR	RDFFE	DEDGK	EYIYKE	PKLT	PLSEIS	QRLL	KLYSDKFGSE	NVKMIQDSGK	VNPKDLDISKY	AYIQVTHVIP	960		
961	FFDEKE	LQER	KTEFER	SHNI	RREMF	EMPFT	QTGKR	QGGVE	EQCKRRTILT	AIHCFPYVKK	RIPVMYQHHT	DLNPIEVAID	1040		
1041	EMSKKV	AEALR	QLCSSA	EVDM	IKLQLK	LQGS	VSVQV	NAGPL	AYARAF	LDNT	NTKRYPD	KNV	KLLKEVFRQF	VEACCGQALAV	1120
1121	NERLIK	EDQL	EYQEEM	KANY	REMAKEL	SEI	MHEQIC	PLEE	KTSVLPNSLH	IFNAISGTPT	STMVHG	MTSS	SSVV	1195	

FIG. 10E (cont.)

	10	20	30	40	50	60	70	80
1	AATTGTAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG	GCCCCCCTC	GAGGTCGACG	GTATCGATAA	GCTTGATATC
81	GAATTCGGCA	CGAGTTTAC	ACCATCACCA	AAACCCAGAA	TTTATGATG	AGATTAAAA	AGAGTTGCC	ACTCAGCTGC
161	ATGAAAAGCA	CCACCTGTTG	CTCACATTCT	TCCATGTCAG	CTGTGACAAC	TCAAGTAAAG	GAAGCAGGAA	GAAGAGGGAT
241	GTCGTTGAAA	CCCAAGTTGG	CTACTCCTGG	CTTCCCCCTC	TGAAAGACGG	AAGGGTGGTG	ACAAGCCAGC	AGCACATCCC
321	GGTCTCGCGG	AACCTTCCCT	CGGGCTATCT	TGGCTACCAA	GAGCTTGGGA	TGGGCAGGCA	TTATGGTCCG	GAAATTAAAT
401	GGGTAGATGG	AGGCAAGCCA	CTGCTGAAAA	TTTCCACTCA	TCTGTTTCT	ACAGGGATAC	TCAGGATCAG	CATTACATA
481	ATTTTTTCCA	GTACTGTGAG	AAAACCGAAT	CTGGAGCCCA	AGCCTTAGGA	AACGAACTTG	TAAAGTACCT	TAAGATCTCG
561	CATGCGATGG	AAGGCCACGT	GATGATCGCC	TTCTTGCCCA	CTATCCTAAA	CCAGCTGTTT	CGAGTCTCTA	CCAGAGCCAC
641	ACAGGAAGAA	GTGCGGGTAA	ACGTGACTCG	GGTCATTATT	CATGTGGTTG	CCCAGTGCCA	TGAGGAAGGA	TTGGAGAGCC
721	ACTTGAGGTC	ATATGTTAAG	TACGCGTATA	AGGCTGAGCC	ATATGTTGCC	TCTGAATACA	AGACATGCA	TGAAGAACTG
801	ACCAAATCCA	TGACCACGAT	TCTCAAGCCT	TCTGCCGATT	TCCTCACCCAG	CAACAAACTA	CTAGGTTACT	CATGGTTTTT
881	CTTTGATGTA	CTGATCAAA	CTATGGCTCA	GCATTTGATA	GAGAACTCCA	AAGTTAAGTT	GCTGCGAAAC	CAGAGATTTC
961	CTGCATCCTA	TCATCATGCA	GCGGAAACCG	TTGTAAATAT	GCTGATGCCA	CACATCACTC	AGAAGTTTGG	GATAATCCA
1041	GAGGCATCTA	AGAACGCGAA	TCATAGCCTT	GCTGTCTTCA	TCAAGAGATG	TTTCACTTTC	ATGGACAGGG	GCTTTGTCTT
1121	CAAGCAGATC	AACAACTACA	TTAGCTGTTT	TGCTCCTGGA	GACCCAAAGA	CCCTCTTTGA	ATACAAGTTT	GAATTTCTCC
1201	GTGTAGTGTG	CAACCATGAA	CATTATATTC	CGTTGAACCT	ACCAATGCCA	TTTGGAAAAG	CGAGGATTC	AAGATACCAA
1281	GACCTCCAGC	TTGACTACTC	ATTAAACAGAT	GAGTTCTGCA	GAAACCACTT	CTTGGTGGGA	CTGTTACTGA	GGGAGGTGGG
1361	GACAGCCCTC	CAGGAGTTCC	GGGAGGTCCG	TCTGATCGCC	ATCAGTGTGC	TCAAGAACCT	GCTGATAAAG	CATTCTTTTG
1441	ATGACAGATA	TGCTTCAAGG	AGCCATCAGG	CAAGGATAGC	CACCCCTTAC	CTGCCCTCTG	TGGTCTGCT	GATTGAAAC
1521	GTCCAGCGGA	TCAATGTGAG	GGATGTGTCA	CCCTTCCCTG	TGAACCGCGG	CATGACCCGT	AAGGATGAAT	CCCTGGCTCT
1601	ACCAGCTGTG	AATCCGCTGG	TGACGCCGCA	GAAGGGAAGC	ACCCTGGACA	ACAGCCTGCA	CAAGGACCTG	CTGGGCGCCA
1681	TCTCCGGCAT	TGCTTCTCCA	TATACAACCT	CAACTCCAAA	CATCAACAGT	GTGAGAAATG	CTGATTCGAG	AGGATCTCTC
1761	ATAAGCACAG	ATTCCGGTAA	CAGCCTTCCA	GAAAGGAATA	GTGAGAAAG	CAATCCCTG	GATAAGCACC	AACAAAGTAG
1841	CACATTGGGA	AATTCCTGGG	TTGCTGTGTA	TAACTTGAC	CAGTCTGAGA	TTAAGAGCCT	ACTGATGTGT	TTCTCTTACA
1921	TCTTAAAGAG	CATGCTGTAT	GATGCTTTGT	TTACATATTG	GAACAAGGCT	TCAACATCTG	AACCTATGGA	TTTTTTTACA
2001	ATATCTGAAG	TCTGCCGTGA	CCAGTTCAG	GATTTCTGGA	AGCGATACAT	AGCCAGGAAC	CAGGAGGGGT	TGGGACCCAT
2081	AGTTTCATGAT	CGAAAGTCTC	AGACATTGCC	TGTTTCCCGT	AACAGAACAG	GAATGATGCA	TGCCAGATTG	CAGCAGCTGG
2161	GCAGCCTGGA	TAACTCTCTC	ACTTTTAAAC	ACAGCTATTG	CCACTCCGAG	GCAGATGTTT	TGCACCAGTC	ATTACTTGAA
2241	GCCAAACATTG	CTACTGAGGT	TTGCCGTGACA	GCTCTGGACA	CGCTTCTCTT	ATTTACATTG	CGCTTTAAGA	ACCAGCTCCT
2321	GGCCGACCAT	GGACATAATC	CTCTCATGAA	AAAAGTTTTT	GATGTCTACC	TGTGTTTCT	TCAAAAACAT	CAGTCTGAAA
2401	CGGCTTTAAA	AAATGTCTTC	ACTGCCCTTAA	GGTCTTAAAT	TTATAAGTTT	CCCTCAACAT	TCTATGAGG	GAGAGCGGAC
2481	ATGTGTGCGG	CTCTGTGTTA	CGAGATTCTC	AAGTGTGTA	ACTCCAAAGT	GAGCTCCATC	AGGACGGAGG	CCTCCCAGCT
2561	GCTCTACTTC	CTGATGAGGA	ACAACTTTGA	TTACTACTGGA	AAGAAGTCTT	TGTCCGGGAC	ACATTTGCAA	GTCTCATAT
2641	CTGTACGCCA	GCTGATAGCA	GACGTTGTTG	GCATTGGGGA	AACAGATTTC	CAGCAGTCCC	TGTCCATCAT	CAACAACATG
2721	GCCAAACAGTG	ACCGGCTTAT	TAAACACACC	AGCTTCTCTT	CTGATGTGAA	GGACTTAAAC	AAAAGGATAC	GCACGGTGCT
2801	AATGGCCACC	GCCCAGATGA	AGGAGCATGA	GAACGACCCA	GAGATGCTGG	TGGACCTCCA	GTACAGCCTG	GCCAAATCCT
2881	ATGCCAGCAC	GCCCCAGCTC	AGGAAGACGT	GGCTCGACAG	CATGGCCAGG	ATCCATGTCA	AAAATGGCGA	TCTCTAGAG
2961	GCAGCAATGT	GCTATGTCCA	CGTAACAGCC	CTAGTGGCAG	ATCTCTCTAC	ACGGAAAGGC	GTGTTTAGAC	AAGGATGCAC
3041	CGCCTTCCAG	GTCATTACCC	CAACATCGA	CGAGGAGGCC	TCCATGATGG	AAGACGTGGG	GATGCAAGAT	GTCCATTCTA
3121	ACGAGGATGT	GCTGATGGAG	CTCCTTGAGC	AGTGGCGAGA	TGGACTCTGG	AAAGCCGAGC	GCTACGAGCT	CATCGCCGAC
3201	ATCTACAAAC	TTATCATCCC	CATTATGAG	AAGCGGAGGG	ATTTCTTTGA	AGATGAAGAT	GGAAAGGAGT	ATATTTCACA
3281	GGAAACCCAAA	CTCACACCGC	TGTCGGAAAT	TTCTCAGAGA	CTCCTTAAAC	TGTACTCGGA	TAAATTGGGT	TCTGAAAATG
3361	TCAAATGAT	ACAGGATTCT	GGCAAGGTCA	ACCCATAAGGA	TCTGGATTCT	AAGTATGCA	ACATCCAGGT	GACTCAGCTC
3441	ATCCCTTCTT	TTGACGAAAA	AGAGTTGCAA	GAAAGGAAAA	CAGAGTTTGA	GAGATCCCA	AACATCCGCC	GCTTCATGTT
3521	TGAGATGCCA	TTTACGCAGA	CCGGGAAGAG	GCAGGGCGGG	GTGGAAGAGC	AGTGCAAAAC	GCGCACCATC	CTGACAGCCA
3601	TACACTGCTT	CCCTTATGTG	AAGAAGCGCA	TCCTGTGATC	GTACCAGCAC	CACACTGACC	TGAACCCCAT	CGAGGTGGCC
3681	ATTGACGAGA	TGAGTAAGAA	GGTGGCGGAG	CTCCGGCAGC	TGTGCTCCTC	GGCCGAGGTG	GACATGATCA	AACTGCAGCT
3761	CAAACTCCAG	GGCAGCGTGA	GTGTTTCAAGT	CAATGCTGGC	CCACTAGCAT	ATGCGCGAGC	TTTCTTAGAT	GATACAAACA
3841	CAAAGCGATA	TCCTGACAAT	AAAGTGAAGC	TGCTTAAAGA	AGTTTTCAGG	CAATTTGTGG	AAGCTTGCGG	TCAAGCCTTA
3921	GCGGTAACG	AACGTCTGAT	TAAAGAAGAC	CAGCTCGAGT	ATCAGGAAGA	AATGAAAGCC	AACACAGGG	AAATGGCGAA
4001	GGAGCTTCT	GAAATCATGC	ATGAGCAGAT	CTGCCCCCTG	GAGGAGAAGA	CGAGCGTCTT	ACCGAATTCC	CTTCACATCT
4081	TCAACGCCAT	CAGTGGGACT	CCAACAAGCA	CAATGGTTCA	CGGGATGACC	AGCTCGTCTT	CGGTCTGTGT	ATTACATCTC
4161	ATGGCCCGTG	TGTGGGGACT	TGCTTTGTCA	TTTGCAAACT	CAGGATGCTT	TCCAAGCCCA	ATCACTGGGG	AGACCGAGCA
4241	CAGGGAGGAC	CAAGGGGAAG	GGGAGAGAAA	GGAAATAAAG	AACAACTGTA	TTTCTTAAAC	GACTTTCTAT	AGGAGTTGTA
4321	AGAAGGTGCA	CATATTTTTT	TAAATCTCAC	TGGCAATATT	CAAAGTTTTC	ATTGTGTCTT	AACAAAGGTG	TGGTAGACAC
4401	TCTTGAGCTG	GACTTAGATT	TTATCTTCTC	TTGCAAGATA	TCTGTAGAA	AGATGGCCTA	CAGAAAAAAA	AGGTTCTGGG
4481	ATCTACATGG	CAGGAGGGGC	TGCACTGACA	TTGATGCCCTG	GGGGACCTTT	TGCTCGACT	CGTGCCGGA	ATCTGATCGT
4561	AATCAGGGTA	CAGAACTTAC	TAGTTTTGTC	TAGGAGTATG	TTGATGACT	AGGATTGTTG	CTATTATCTC	ATCAACCAAC
4641	ATAGAGCAAG	AATAGTGAGC	TAACTGAGCT	AGACACTCAA	TTAATCCGCT	ACTGGCTTCA	AGTCAGAACT	TTGTCAATTA
4721	TCATCGACTC	CGGGACGGTC	ATATATGTAT	TACATTCTTA	CATTTTTAAT	ACTCACATGG	GCTTATGCAT	TAAGTTTAAAT
4801	TGTATAAAT	TTGTGCTGGT	CCAGTATATG	CAATACACTT	TAATGGTTTA	TTCTTGTCAT	AAAAATGTGC	AATATGGAGA
4881	TGTATACAAG	TCTTTACT						4898

FIG.10F

		10		20		30		40			50		60		70		80	
1	MEGHVMIAFL	PTILNQLFRV	LTRATQEEVA	VNVTRVIIHV	VAQCHEEGLE	SHLRSYVKYA	YKAEPYVASE	YKTVHEELTK	80									
81	SMTILKPSA	DELTSENKLLR	YSWFFFDVLI	KSMAQH LIEN	SKVKLLRNQR	FPASYHHAAE	TVVNMLMPHI	TQKFGDNPEA	160									
161	SKNANHSLAV	FIKRCFTFMD	RGFVFKQINN	YISCFAPGDP	KTLEFYKFEF	LRVVCNHEHY	IPINLPMPPFG	KGRIQRYQDL	240									
241	QLDYSLTDEF	CRNHFLVGLL	LREVG TALQE	FREVRLIAIS	VLKNLLIKHS	FDDRYASRSH	QARIATLYLP	LFGLLIENVQ	320									
321	RINVRDVSPF	PVNAGMTVKD	ESLALPAVNP	LVTPOKGSTL	DNSLHKDILG	AISGIASPYT	TSTPNINSVR	NADSRGSLIS	400									
401	TDSGNSLPER	NSEKSNSLDK	HQQSSTLGNS	VVRCDKLDQS	EIKSLIMCFL	YILKSMSDDA	LFTYWNKAST	SELMDFFTIS	480									
481	EVCLHQFQYM	GKRYIARNQE	GLGPIVHDRK	SQTLFVSRNR	TGMMHARLQQ	LGSLDNSLTF	NHSYGHSDAD	VLHQSLLEAN	560									
561	IATEVCLTAL	DTLSLETLAF	KNQLLADHGH	NPLMKKVFDV	YLCFLQKHQS	ETALKNVFTA	LRS LIYKFPS	TFYEGRADMC	640									
641	AALCYEILKC	CNSKLS SIRT	EASQLLYFILM	RNNFDYTGKK	SFVRTHLQVI	ISVSQ LIADV	VGIGETRFQQ	SLSIINN CAN	720									
721	SDRLIKHTSF	SSDVKD LTKR	IRTVLMATAQ	MKEHENDPEM	LVDLQYSLAK	SYASTPELRK	TWLD SMARIH	VKNGDLSEAA	800									
801	MCYVHV TALV	AEYLTRKGVF	RQGCTAFRVI	TPNIDEEASM	MEDVGMQDVH	FNEDVLMELL	EQCADGLWKA	ERYELIADIY	880									
881	KLIIP IYEKR	RDFFEDEDGK	EYIYKEPKLT	PLSEISQRLI	KLYSDKFGSE	NVKMIQDSGK	VNPKOLD SKY	AYIQVTHVIP	960									
961	FFDEKELQER	KTEFERSHNI	RRFMFEMPFT	QTGKRQGGVE	EQCKRRTILT	AIHCFPYVKK	RIPVMYQHHT	DLNPIEVAID	1040									
1041	EMSKKVAELR	QLCSSAEVDM	IKLQLKLQGS	VSVQVNAGPL	AYARAFLDDT	NTKRYPDNKV	KLLKEVFRQF	VEACGQALAV	1120									
1121	NERLIKEDQL	EYQEEMKANY	REMAKELSEI	MHEQICPLEE	KTSVLENSLH	IFNAISGTPT	STMVHGMTSS	SSVV	1195									
		10		20		30		40			50		60		70		80	

FIG. 10F (cont.)

	10	20	30	40	50	60	70	80	
1	AATTGTAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG	GCCCCCCTC	GAGGTCGACG	GTATCGATAA	GCTTGATATC	80
81	GAATTCCGCA	CGAGTTTAC	ACCATCACCA	AAACCCAGAA	TTTATGATG	AGATTAATAA	AGAGTTGCC	ACTCAGCTGC	160
161	ATGAAAAGCA	CCACCTGTTG	CTCACATTCT	TCCATGTTCAG	CTGTGACAA	TCAAGTAAAG	GAAGCAGCAA	GAAGAGGGAT	240
241	GTCGTTGAAA	CCCAAGTTGG	CTACTCCTGG	CTTCCCTCC	TGAAAGACGG	AAGGTTGGTG	ACAAGCGAGC	AGCACATCCC	320
321	GGTCTCGGCG	AACCTTCCTT	CGGGCTATCT	TGGCTACCAA	GAGCTTGGGA	TGGGCAGGCA	TTATGGTCCG	GAAATTAAT	400
401	GGGTAGATGG	AGGCAAGCCA	CTGCTGAAAA	TTTCCACTCA	TCTGGTTTCT	ACAGGGATAC	TCAGGATCAG	CATTACATA	480
481	ATTTTTCCTA	GTACTGTTCAG	AAAACCGAAT	CTGGAGCCCC	AGCCTTAGGA	AACGAACTTG	TAAAGTACCT	TAAGAGTCTG	560
561	CATGCGATGG	AAGGCCACGT	GATGATCGCC	TTCTTGCCCC	CTATCCTAAA	CCAGCTGTTT	CGAGTCCCTA	CCAGAGCCAC	640
641	ACAGGAAGAA	GTCGCGGTTA	ACGTGACTCG	GGTCATTATT	CATGTGGTTG	CCCAGTGCCA	TGAGGAAGGA	TTGGAGAGCC	720
721	ACTTGAGGTC	ATATGTTAAG	TACGCGTATA	AGGCTGAGCC	ATATGTTGCC	TCTGAATACA	AGACAGTGCA	TGAAGAACTG	800
801	ACCAAATCCA	TGACCACGAT	TCTCAAGCCT	TCTGCCGATT	TCCTCAACAG	CAACAACTA	CTGAGGTACT	CATGGTTTTT	880
881	CTTTGATGTA	CTGATCAAAT	CTATGGCTCA	GCATTTGATA	GAGAAGTCCA	AAGTTAAGTT	GCTGCCAAAC	CAGAGATTTT	960
961	CTGCATCCTA	TCATCATGCA	GCGGAAACCG	TTGTAAATAT	GCTGATGCCA	CACATCACTC	AGAAGTTTGG	AGATAATCCA	1040
1041	GAGGCATCTA	AGAACGCGAA	TCATAGCCTT	GCTGTCTTCA	TCAAGAGATG	TTTACCTTTC	ATGGACAGGG	GCTTTGTCTT	1120
1121	CAAGCAGATC	AACAACATCA	TTAGCTGTTT	TGCTCCTGGA	GACCCAAAGA	CCCTCTTTGA	ATACAAGTTT	GAATTTCTCC	1200
1201	GTGTAGTGTG	CAACCATGAA	CATTATATTC	CGTTGAACCT	ACCAATGCCA	TTTGGAAAAAG	GCAGGATTCA	AAGATACCAA	1280
1281	GACCTCCAGC	TTGACTACTC	ATTAACAGAT	GAGTTCTGCA	GAACCAACTT	CTTGGTGGGA	CTGTACTGA	GGGAGGTGGG	1360
1361	GACGAGCCTC	CAGGAGTTCC	GGGAGGTCGG	TCTGATCGCC	ATCAGTGTGC	TCAAGAACCT	GCTGATAAAG	CATTCTTTTG	1440
1441	ATGACAGATA	TGCTTCAAGG	AGCCATCAGG	CAAGGATAGC	CACCTCTTAC	CTGCCTCTGT	TTGGTCTGCT	GATTGAAAAA	1520
1521	GTCGAGCGGA	TCAATGTGAG	GGATGTGTCA	CCCTTCCCTG	TGAACGCGGG	CATGACCGTG	AAGGATGAAT	CCCTGGCTCT	1600
1601	ACCAGCTGTG	AATCCGCTGG	TGACGCCGCA	GAAGGGAAGC	ACCCTGGACA	ACAGCCTGCA	CAAGGACCTG	CTGGCGGCCA	1680
1681	TCTCCGGCAT	TGCTTCTCCA	TATACAACCT	CAACTCCAAA	CATCAACAGT	GTGAGAAATG	CTGATTTCAG	AGGATCTCTC	1760
1761	ATAAGCAGAG	ATTCGGGTAA	CAGCCTTCCA	GAAGGAATA	GTGAGAAGAG	CAATTCCCTG	GATAAGCACC	AACAAAGTAG	1840
1841	CACATTGGGA	AATTCGCTGG	TTGCTGTGTA	TAAACTTGAC	CAGTCTGAGA	TTAAGAGCCT	ACTGATGTGT	TTCTCTTACA	1920
1921	TCTTAAAGAG	CATGCTGTAT	GATGCTTTGT	TTACATATTG	GAACAAGGCT	TCAACATCTG	AACCTTATGA	TTTTTTTACA	2000
2001	ATATCTGAAG	TCTGCCTGCA	CCAGTTCAG	TACATGGGGA	AGCCATACAT	AGCCAGGAAC	CAGGAGGGGT	TGGAGCCCAT	2080
2081	AGTTACATGAT	GCAGAGTCTC	AGACATTGCC	TGTTTCCCGT	ACAGAAACAG	GAATGATGCA	TGCCAGATTG	CAGCAGCTGG	2160
2161	GCAGCCTGGA	TAACTCTCTC	ACTTTTAAAC	ACAGCTATGG	CCACTCGGAC	GCAGATGTTT	TGCACAGATC	ATTACTTGAA	2240
2241	GCCAAATATG	CTACTGAGGT	TTGCTTGACA	GCTCTGGACA	CGCTTTCTCT	ATTTACATTG	CGGTTTAAAG	ACCAGCTCCT	2320
2321	GGCCGACCAT	GGACATAATC	CTCTCATGAA	AAAAGTTTTT	GATGCTTACC	TGTGTTTTCT	TCAAAAACAT	CAGTCTGAAA	2400
2401	CGGCTTTAAA	AAATGTCTTC	ACTGCCTTAA	GGTCTTAAAT	TTATAAGTTT	CCCTCAACAT	TCTATGAAGG	GAGAGCGGAC	2480
2481	ATGTGTGCGG	CTCTGTGTTA	CGAGATTCTC	AAGTGTCTGA	ACTCCAAGCT	GAGCTCCATC	AGGACGGAGG	CCTCCAGCTT	2560
2561	GCTCTACTTC	CTGATGAGGA	ACAACTTTGA	TTACACTTGA	AAGAAGTCTT	TTGTCGGGAC	ACATTTGCAA	GTCATCATAT	2640
2641	CTGTACGCCA	GCTGATAGCA	GACGTGTTTG	GCATTGGGGA	AACAGATGTC	CAGCAGTCCC	TGTCCATCAT	CAACAACCTG	2720
2721	GCCAAACAGT	ACCGGCTTAT	TAAGCACACC	AGCTTCTCCT	CTGATGTGAA	GGACTTAAAC	AAAGGATAC	GCACGGTGCT	2800
2801	AATGGCCACC	GCCAGATGA	AGGAGCATGA	GAACGACCCA	GAGATGCTGG	TGGACCTCCA	GTACAGCCTG	GCCAAATCCT	2880
2881	ATGCCAGCAC	GCCCGAGCTC	AGGAAGACGT	GGCTCGACAG	CATGGCCAGG	ATCCATGTCA	AAAATGGCGA	TCTCTCAGAG	2960
2961	GCAGCAATGT	GCTATGTCCA	CGTAACAGCC	CTAGTGGGCA	AATATCTCAC	ACGGAAAGGC	GTGTTTAGAC	AAGGATGCAC	3040
3041	CGCCTTCAGG	GTCATTACCC	CAAAACATCGA	CGAGGAGGCC	TCCATGATGG	AAGACGTGGG	GATGCAGGAT	GTCATTTCAT	3120
3121	ACGAGGATGT	GCTGATGGAG	CTCCTTGAGC	AGTGCGCAGA	TGGACTCTGG	AAAGCCGAGC	GCTACGAGCT	CATCGCCGAC	3200
3201	ATCTACAAAC	TTATCATCCC	CATTTATGAG	AAGCGGAGGG	ATTTCTTTGA	AGATGAAGAT	GGAAAGGAGT	ATATTTCACA	3280
3281	GGAAACCCAA	CTCACACCCG	TGTCGGAAAT	TTCTCAGAGA	CTCCTTAAAC	TGTACTCGGA	TAAATTGTTT	TCTGAAAATG	3360
3361	TCAAAATGAT	ACAGGATTCT	GGCAAGGTCA	ACCTAAAGGA	TCTGGATTCT	AAGTATGCAT	ACATCCAGGT	GACTCACGCT	3440
3441	ATCCCTTCTT	TTGACGAAAA	AGAGTTGCAA	GAAGGAAAAA	CAGAGTTTGA	GAGATCCAC	AACATCCGCC	GCTTCATGTT	3520
3521	TGAGATGCCA	TTTACGCAGA	CCGGGAAGAG	GCAGGCGGGG	GTGGAAGAGC	AGTGCAAACG	GCGCACCATC	CTGACAGCCA	3600
3601	TACACTGCTT	CCCTTATGTG	AAGAAGCGCA	TCCCTGTCTAT	GTACCAGCAC	CACACTGACC	TGAACCCCAT	CGAGGTGGCC	3680
3681	ATTGACGAGA	TGAGTAAGAA	GGTGGCGGAG	CTCCGGCAGC	TGTGCTCTCT	GGCCGAGGTG	GACATGATCA	AACTGCAGCT	3760
3761	CAAACTCCAG	GGCAGCGTGA	GTGTTCAGGT	CAATGCTGGC	CCACTAGCAT	ATGCGCGAGC	TTTCTTAGAT	GATACAAACA	3840
3841	CAAAGCGATA	TCCTGACAAAT	AAAGTGAAGC	TGCTTAAAGGA	AGTTTTTCAGG	CAATTTGTGG	AAGCTTGGCG	TCAAGCCTTA	3920
3921	GCGGTAAACG	AACGTCTGAT	TAAAGAAGAC	CAGCTCGAGT	ATCAGGAAGA	AATGAAAGCC	AACACAGGG	AAATGGCGAA	4000
4001	GGAGCTTTCT	GAAATCATGC	ATGAGCAGAT	CTGCCCCCTG	GAGGAGAAGA	CGAGCGTCTT	ACCGAATTCC	CTTCACATCT	4080
4081	TCAACGCCAT	CAGTGGGACT	CCAACAAGCA	CAATGGTTCA	CGGGATGACC	AGCTCGTCTT	CGGTCTGTGT	ATTACATCTC	4160
4161	ATGGCCCCGTG	TGTGGGGACT	TGCTTTGTCA	TTTGCAAACT	CAGGATGCTT	TCCAAAGCCA	ATCACTGGGG	AGACCGAGCA	4240
4241	CAGGGAGGAC	CAAGGGGAAG	GGGAGAGAAA	GGAAATAAAG	AACAACGTTA	TTTCTTAAAC	GACTTTCTAT	AGGAGTTGTA	4320
4321	AGAAGGTGCA	CATATTTTTT	TAAATCTCAC	TGGCAATATT	CAAGATTTTC	ATTGTGCTCT	AACAAAGGTG	TGGTAGACAC	4400
4401	TCTTGAGCTG	GACTTAGATT	TTATTCTTCC	TTGCAGAGTA	GTGTTAGAA	AGATGGCCTA	CAGAAAAAAA	AGGTTCTGGG	4480
4481	ATCTACATGG	CAGGAGGGGC	TGCACGTGCA	TTGATGCTTG	GGGGACCTTT	TGCCTCGACT	CGTGCCGAAA	ATCTGATCGT	4560
4561	AATCAGGGTA	CAGAAGTTAC	TAGTTTTGTC	TAGGAGTATG	TTGTATGACT	AGGATTGTGT	CTATATCTCT	ATTCAACAAC	4640
4641	ATAGAGCAAG	AATAGTGAGC	TAACTGAGCT	AGACACTCAA	TTAATCCGCT	ACTGGCTTCA	AGTCAGAACT	TTGTCAATTA	4720
4721	TCATCGACTC	CGGGACGGTC	ATATATGTAT	TACATTTCTA	CATTTTTAAT	ACTCACATGG	GCTTATGCAT	TAAGTTTAAAT	4800
4801	TGTGATAAAT	TTGTGCTGGT	CCAGTATATG	CAATACACTT	TAATGGTTTA	TTCTTGTCTAT	AAAAATGTGC	AATATGGAGA	4880
4881	TGTATACAAG	TCTTTACT							4898

FIG.10G

	10	20	30	40	50	60	70	80
1	MEGHVMI AFL	PTILNQLFRV	LTRATQEEVA	VNVTRV I I HV	VAQCHEEGLE	SHLSYVKYA	YKAEPYVASE	YKTVHEELTK 80
81	SMTILKPSA	DFLT SNKLLR	YSWFFFDVLI	KSMAQH LIEN	SKVKLLRNQR	FPASYHHAAE	TVVNM LMPHI	TQKFGDNPEA 160
161	SKNANHSLAV	FIKRCFTFMD	RGFVFKQINN	YISCFAPGDP	KTLFFEYKFEF	LRVVCNHEHY	IPLNLPMPFG	KGRIQRYQDL 240
241	QLDYSLTDEF	CRNHFLVGLL	LREVG TALQE	FREVRLIAIS	VLKNLLIKHS	FDDRYASRSH	QARIATLYLP	LFGLLIENVQ 320
321	RINVRDVSEF	PVNAGMTVKD	ESLALPAVNP	LVTPQKGSTL	DNSLHKDLLG	AISGIASPYT	TSTPNINSVR	NADSRGSLIS 400
401	TDSGNSLPER	NSEKSNSLDK	HQQSSTLGNS	VVRCDKLDQS	EIKSLLMCFI	YILKMSDDA	LEFTYWNKAST	SEIMDEFTIS 480
481	EVCLHQFQYM	GKRYIARNQE	GLGP I VHDRK	SQTLFVSRNR	TGMMHARLQQ	LGSLD NSLTF	NHSYGHSDAD	VLHQSLLEAN 560
561	IATEVCLTAL	DTLSLFTLAF	KNQLLADHGH	NPLMKKVFDV	YLCFLQKHQS	ETALKNVETA	LRLIYKFPS	TFYEGRADMC 640
641	AALCYEILKC	CNSKLSSIRT	EASQLLYFLM	RNNFDYTGKK	SEVTRTHLQVI	ISVSQLIADV	VGIGETRFQQ	SLSIINN CAN 720
721	SDRLIKHTSF	SSDVKDLTKR	IRTVLMATAQ	MKEHENDPEM	LVDLQYSLAK	SYASTPELRK	TWLD SMARIH	VKNGDLSEAA 800
801	MCYVHV TALV	AEYLTRKGVF	RQGCTAFRVI	TPNIDEEASM	MEDVGMQDVH	FNEDVLMELL	EQCADGLWKA	ERYELIADIY 880
881	KLIIP IYEKR	RDFFEDEDGK	EYIYKEPKLT	PLSEISQRLL	KLYSDKFGSE	NVKMIQDSGK	VNPKDLDSKY	AYIQVTHVIP 960
961	FFDEKELQER	KTEFERSHNI	RRFMFEMPFT	QTGKRQGGVE	EQCKRRTILT	AIHCFPYVKK	RIPVMYQHHT	DINPIEVAID 1040
1041	EMSKKVAELR	QLCSSAEVDM	IKLQLKLQGS	VSVQVNAGPL	AYARAF LDDT	NTKRYPDNKV	KLLKEVFRQF	VEACGQALAV 1120
1121	NERLIKEDQL	EYQEEMKANY	REMAKELSEI	MHEQICPLEE	KTSVLPNSLH	IFNAISGTPT	STMVHGMTSS	SSVV 1195

FIG. 10G (cont.)

	10	20	30	40	50	60	70	80
1	AATTGTAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG	GGGGGGCTC	GAGGTCGACG	GTATCGATAA	GCTTGATATC 80
81	GAATTCGGCA	CGAGTTTAC	ACCATCACCA	AAACCCAGAA	TTTTATGATG	AGATTAAAAA	AGAGTTGCCC	ACTCAGCTGC 160
161	ATGAAAAGCA	CCACCTGTTG	CTCACATTCT	TCCATGTCAG	CTGTGACAAC	TCAAGTAAAG	GAAGCACGAA	GAAGAGGGAT 240
241	GTCGTTGAAA	CCCAAGTTGG	CTACTCCTGG	CTTCCCTTCC	TGAAAGACGG	AAGGGTGGTG	ACAAGCGAGC	AGCACATCCC 320
321	GGTCTCGGCG	AACTTTCCTT	CGGGCTATCT	TGGCTACCAA	GAGCTTGGGA	TGGGCAGGCA	TTATGGTCCG	GAAATTAAT 400
401	GGGTAGATGG	AGGCAAGCCA	CTGCTGAAAA	TTTCCACTCA	TCTGGTTTCT	ACAGGGATAC	TCAGGATCAG	CATTACATA 480
481	ATTTTTTCCA	GTACTGTCAG	AAAACCGAAT	CTGGAGCCCC	AGCCTTAGGA	AACGAACTTG	TAAAGTACCT	TAAGAGTCGG 560
561	CATGCCATGG	AAGGCCACGT	GATGATCGCC	TTCTTGCCCC	CTATCCTAAA	CCAGCTGTTT	CGAGTCTCTA	CCAGAGCCAC 640
641	ACAGGAAGAA	GTGCGGGTTA	ACGTGACTCG	GGTCATTATT	CATGTGGTTG	CCCAGTGCCA	TGAGGAAGGA	TTGGAGAGCC 720
721	ACTTGAGGTC	ATATGTTAAG	TACGCGTATA	AGGCTGAGCC	ATATGTTGCC	TCTGAATACA	AGACAGTGCA	TGAAGAACTG 800
801	ACCAAATCCA	TGACCACGAT	TCTCAAGCCT	TCTGCCGATT	GAGAACTCCA	AAGTTAAGTT	GCTGCGAAAC	CAGAGATTTC 960
881	CTTTGATGTA	CTGATCAAAAT	CTATGGCTCA	GCATTTGATA	GCTGATGCCA	CACATCACTC	AGAAGTTTGG	CAGATTAATCCA 1040
961	CTGCATCCTA	TCATCATGCA	GCGGAAACCG	TTGTAAATAT	TCTCACCCAG	CAACAAACTA	CTGAGGTACT	CATGGTTTTT 880
1041	GAGGCATCTA	AGAAGCGGAA	TCATAGCCTT	GCTTGCCCA	GAGAACTCCA	AAGTTAAGTT	GCTGCGAAAC	CAGAGATTTC 960
1121	CAAGCAGATC	AACAACCTACA	TTAGCTGTTT	TGCTCCTGGA	TCTCACCCAG	CAACAAACTA	CTGAGGTACT	CATGGTTTTT 880
1201	GTGTAGTGTG	CAACCATGAA	CATTATATTC	CGTTGAACTT	TCAAGAGATG	TTTCACTTTC	ATGGACAGGG	GCTTTGTCTT 1120
1281	GACCTCCAGC	TTGACTACTC	ATTAACAGAT	GAGTTCTGCA	GACCCAAAGA	CCCTCTTTGA	ATACAAGTTT	GAATTTCTCC 1200
1361	GACAGCCCTC	CAGGAGTTCC	GGGAGGTCCG	TCTGATCGCC	ACCAATGCCA	TTTGGAAAAG	CGAGGATTCA	AAGATACCAA 1280
1441	ATGACAGATA	TGCTTCAAGG	AGCCATCAGG	CAAGGATAGC	AGCAACCACTT	CTTGGTGGGA	CTGTTACTGA	GGGAGGTGGG 1360
1521	GTCCAGCGGA	TCAATGTGAG	GGATGTGTCA	CCCTTCCCCT	ATCAGTGTGC	TCAAGAACCT	GCTGATAAAG	CATTCTTTTG 1440
1601	ACCAAGCTGT	AATCCGCTGG	TGACGCCGCA	GAAGGGAAGC	CACCCCTCTAC	CTGCCCTCTG	TTGGTCTGCT	GATTGAAAAC 1520
1681	TCTCCGGCAT	TGCTTCTCCA	TATACAACCT	CAACTCCAAA	TGAACCGGGG	CATGACCGTG	AAGGATGAAT	CCCTGGCTCT 1600
1761	ATAAGCACAG	ATTCCGGTAA	CAGCCTTCCA	GAAGGGAATA	ACCCTGGACA	ACAGCCTGCA	CAAGGACCTG	CTGGGCGCCA 1680
1841	CACATTGGGA	AATTCGGTGG	TTGCTGTGTA	TAACTTGAC	CATCAACAGT	GTGAGAAATG	CTGATTCGAG	AGGATCTCTC 1760
1921	TCTTAAAGAG	CATGCTGAT	GATGCTTTGT	TTACATATTG	GTGAGAAAGAG	CAATTCCTTG	GATAAGCACC	AACAAAGTAG 1840
2001	ATATCTGAAG	TGCTCCTGCA	CCAGTTCAGG	TACATGGGGA	CAGTCTGAGA	TTAAGAGCCT	ACTGATGTGT	TTCTCTCTAC 1920
2081	AGTTCATGAT	CGAAAGTCTC	AGACATTGCC	TGTTTCCCGT	GAACAAGGCT	TCAACATCTG	AACTTATGGA	TTTTTTTACA 2000
2161	GCAGCCTGGA	TAACTCTCTC	ACTTTTAACC	ACAGCTATGG	AGCGATACAT	AGCCAGGAAC	CAGGAGGGGT	TGGGACCCAT 2080
2241	GCCAACATTG	CTACTGAGGT	TTGCTTGACA	GCTCTGGACA	AACAGAACAG	GAATGATGCA	TGCCAGATTG	CAGCAGCTGG 2160
2321	GGCCGACCAT	GGACATAATC	CTCTCATGAA	AAAAGTTTTT	CCACTCGGAC	GCAGATGTTT	TGCACCTAT	TTACTTTGAA 2240
2401	CGGCTTTAAA	AAATGTCTTC	ACTGCCTTAA	GGTCTTTAAT	CGCTTCTCTC	ATTTACATTG	CGGTTTAAAG	ACCAGCTCCT 2320
2481	ATGTGTGCGG	CTGTGTGTTA	CGAGATTCTC	AAGTGTGTTA	GATGTCTACC	TGTGTTTTCT	TCAAAAACAT	CAGTCTGAAA 2400
2561	GCTCTACTTC	CTGATGAGGA	ACAACCTTGA	TTACACTGGA	TTATAAGTTT	CCCTCAACAT	TCTATGAAG	GAGATCTCTC 2480
2641	CTGTACAGCA	GCTGATAGCA	GACGTGTTG	GCATTGGGGA	ATCCAAAGCT	GAGCTCCATC	AGGACGGAGG	CCTCCCAGCT 2560
2721	GCCAACAGTG	ACCGGCTTAT	TAAGCACACC	AGCTTCTCCT	AACAGATTTC	CAGCAGTCCC	TGCTCCATAT	CAACACTGT 2720
2801	AATGGCCACC	GCCCAGATGA	AGGAGCATGA	GAACGACCCA	ATCCGATATC	CAGCAGTCCC	AAAAGGATAC	GCACGGTGCT 2800
2881	ATGCCAGCAC	CGCCGAGCTC	AGGAAGACGT	GGCTCGACAG	GAGATGCTGG	TGGACCTCCA	GTACAGCCTG	GCCAAATCCT 2880
2961	CGCCAAATGT	GCTATGTCCA	CGTAACAGCC	CTAGTGGCAG	CATGGCCAGG	ATCCATGTCA	AAAATGGCCA	TCTCTCAGAG 2960
3041	CGCCTTCAGG	GTCATTACCC	CAAACATCGA	CGAGGAGGCC	AATATCTCAC	ACGGAAGGCG	GTGTTTAGAC	AAGGATGCAC 3040
3121	ACGAGGATGT	GCTGATGGAG	CTCCTTGAGC	AGTGCGCAGA	TCCATGATGG	AAGACGTGGG	GATGCAAGGT	GTCCATTTC 3120
3201	ATCTACAAAC	TTATCATCCC	CATTTATGAG	AAGCGGAGGG	TGGACTCTGG	AAAGCCGAGC	GCTACGAGCT	CATCGCCGAC 3200
3281	GGAAACCCAA	CTCACACCCG	TGTCGGAAAT	TTCTCAGAGA	ATTTCTTTGA	AGATGAAGAT	GGAAAGGAGT	ATATTTTACA 3280
3361	TCAAAATGAT	ACAGGATTCT	GGCAAGGTCA	ACCCTAAGGA	CTCCTTAAAC	TGTAATCGGA	TAAATTTGGT	TCTGAAAATG 3360
3441	ATCCCTTTCT	TTGACGAAAA	AGAGTTGCAA	GAAGGAAAAA	TCTGGATTCT	AAGTATGCAT	ACATCCAGGT	GACTCACGTC 3440
3521	TGAGATGCCA	TTTACGCGA	CCGGGAAGAG	CGAGGGCGGG	CAGAGTTTGA	GAGATCCCAC	AACATCCGCC	GCTTCATGTT 3520
3601	TACTACTGCT	CCCTTATGTG	AAGAAGCGCA	TCCCTGTCTAT	GTGGAAGAGC	AGTGCAAAAC	CGCGACCATC	CTGACAGCCA 3600
3681	ATACTGCTGT	TGAGTAAGAA	GGTGGCGGAG	CTCCGCGCAG	GTACCAGCAC	CACACTGACC	TGAACCCCAT	CGAGGTGGCC 3680
3761	CAAACCTCCAG	GGCAGCGTGA	GTGTTCCAGT	CAATGCTGGC	TGTGCTCCTC	GGCCGAGGTG	GACATGATCA	AACTGCAGCT 3760
3841	CAAAGCGATA	TCCTGACAAT	AAAGTGAAGC	TGCTTAAAGG	CCACTAGCAT	ATGCGCGAGC	TTTCTTAGAT	GATACAAACA 3840
3921	GGCGTAAACG	AACGTCTGAT	TAAAGAAGAC	CAGCTCGAGT	AGTTTTCAGG	CAATTGTGCG	AAGCTTGCGG	TCAAGCCTTA 3920
4001	GCGAGCTTTCT	GAATCATGCT	ATGAGCAGAT	CTGCCCCCTG	ATCAGGAAGA	AATGAAAGCC	AACTACAGGG	AAATGGCGAA 4000
4081	TCAACGCCAT	CAGTGGGACT	CCAACAAGCA	CAATGGTTCA	GAGGAGAAGA	CGAGCGTCTT	ACCGAATTCC	CTTCACATCT 4080
4161	ATGGCCCCGTG	TGTGGGGACT	TGCTTTGTCA	TTTGCAAAAT	CGGGATGACC	AGCTCGTCTT	CGGTCTGTGT	ATTACATCTC 4160
4241	CAGGGAGGAC	CAAGGGGAAG	GGGAGAGAAA	GGAAATAAAG	CAGGATGCTT	TCCAAAGCCA	ATCACTGGGG	AGACCGAGCA 4240
4321	AGAAGGTGCA	CATATTTTTT	TAAATCTCAC	TGGCAATATT	AACAACGTTA	TTTCTTAAAC	GACTTTCTAT	AGGAGTTGTA 4320
4401	TCTTGAAGCTG	CAGTTAGATT	TTATTCTTCC	TTGCAGAGTA	CAAAGTTTTT	ATTGTGTCTT	AACAAGGTG	TGGTAGACAC 4400
4481	ATCTACATGG	CAGGGAGGGC	TGCACTGACA	TTGATGCTGT	GGGGACCTTT	TGCCCTCGAT	CGTGCCGGAA	ATCTGATCGT 4560
4561	AATCAGGGTA	CAGAACCTTAC	TAGTTTTGTC	TAGGAGTATG	TTGTATGACT	AGGATTGTGT	CTATTATCTC	ATTCAACAAC 4640
4641	ATAGAGCAAG	AATAGTGAGC	TAACTGAGCT	AGACACTCAA	TTATCCCGCT	ACTGGCTTCA	AGTCAGAACT	TTGTCAATTAA 4720
4721	TCATCGACTC	CGGGACGGTC	ATATATGTAT	TACATTTCTA	CATTTTAAAT	ACTCACATGG	GCTTATGCAT	TAAGTTTAAAT 4800
4801	TGTGATAAAT	TTTGCTGTGT	CCAGTATATG	CAATACACTT	TAATGGTTTA	TTCTTGTCAT	AAAAATGTGC	AATATGGAGA 4880
4881	TGTATACAAG	TCTTTACT						4898

FIG.10H

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	10	20	30	40	50	60	70	80				
1	MEGHVMI	FLPTI	LNQLFRV	LTRATQEEVA	VNVTRV	IIHV	VAQCHEEGLE	SHLRSYVKYA	YKAEPYVASE	YKTVHEELTK	80	
81	SMTTILKPSA	DELT	SNKLLR	YSWFFFDVLI	KSMAQH	LLEN	SKVKLLRNQR	FPASYHHAAE	TVVNM	LMPHI	TQKFGDNPEA	160
161	SKNANHSLAV	FIKRCFT	FMD	RGFVFKQINN	YISCFAP	GDP	KTLFEYKFEF	LRVVCNHEHY	IPLN	LMPFG	KGRIQRYQDL	240
241	QLDYSLTDEF	CRNHFLV	GLL	LREVGTA	LQE	FREVRLIAIS	VLKNLLIKHS	FDDRYASRSH	QARIATLYLP	LFGLLIENVQ	320	
321	RINVRDVSPF	PVNAGMTVKD	ESLALPAVNP	LVTPQKGSTL	DNSLHKDLLG	AISGIASPYT	TSTPNINSVR	NADSRGSLIS	400			
401	TDSGNSLPER	NSEKSN	SLDK	HQQSSTLGNS	VVRCDKLDQS	EIKSLLMCFL	YILKMSDDA	LFTYWNKAST	SELMDFFTIS	480		
481	EVCLHQFQYM	GKRYIARNQE	GLGPIVHDRK	SQTLFVSRNR	TGMHARLQQ	LGSLD	NSLTF	NHSYGHSDAD	VLHQSLLEAN	560		
561	IATEVCLTAL	DTLSLFTLAF	KNQLLADHGH	NPLMKKVFDV	YLCFLQKHQS	ETALKNVFTA	LRSLIYKFPS	TFYEGRADMC	640			
641	AALCYEILKC	CNSKLSSIRT	EASQLLYFLM	RNNFDYTGKK	SEVTRHLQVI	ISVSQ	LIADV	VGIGETREFQQ	SLSIINN	CAN	720	
721	SDRLIKHTSF	SSDVKD	LTKR	IRTVLMATAQ	MKEHENDP	FEM	LVDLQYSLAK	SYASTPELRK	TWLD	SMARIH	VKNGDLSEAA	800
801	MCYVHV	TALV	AEYLTRKGVF	RQGC	TAFRVI	TPNIDEEASM	MEDVGMQDVH	FNEDVLMELL	EQCADGLWKA	ERYELIADIY	880	
881	KLIIP	PIYEKR	RDFFEDEDGK	EYIYKEPKLT	PLSEISQRL	L	KLYSDKFGSE	NVKMIQDSGK	VNPKD	LDSKY	AYIQVTHVIP	960
961	FFDEKELQER	KTEFERSHNI	RRFMFEMPFT	QTGKRQGGVE	EQCKRRTILT	AIHCFPYVKK	RIPVMYQHHT	DLNPIEVAID	1040			
1041	EMSKKVAELR	QLCSSAEVDM	IKLQLKLQGS	VSVQVNAGPL	AYARAFLDDT	NTKRYPDNKV	KLLKEVFRQF	VEACGQALAV	1120			
1121	NERLIKEDQL	EYQEEMKANY	REMAKELSEI	MHEQICPLEE	KTSVLPNSLH	IFNAISGTPT	STMVHG	MTSS	SSVV	1195		

FIG. 10H (cont.)